



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 178168

TO: Bao-Qun Li
Location: REM-3D24&3C18
Art Unit: 1648
Thursday, February 09, 2006
Case Serial Number: 10/817591

From: Toby Port
Location: Biotech-Chem Library
REM-1A59
Phone: 571-272-2523

toby.port@uspto.gov

Search Notes

Examiner Li,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Toby Port
X22523

6680059

16,719,619

6960569

6858590 09/929, 958

09/705,547

09/466,035

08/931,031





STIC SEARCH RESULTS FEEDBACK FORM

Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher* or *contact*:

Mary Hale, Information Branch Supervisor
Remsen Bldg. 01 D86
571-272-2507

Voluntary Results Feedback Form

➤ I am an examiner in Workgroup: Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC-Biotech-Chem Library, Remsen Bldg.



1033.1.2013

STIC-Biotech/ChemLib

178168

From: Li, Bao-Qun
Sent: Tuesday, January 31, 2006 12:59 PM
To: STIC-Biotech/ChemLib
Subject: 10,817,591

Please do the sequence homology and interference search for SEQ ID NO: 16 and its complement.

Bao Qun Li M.D
TC 1600
Art Unit 1648
Tel. 517-272-0904
REM, 3C18
Rm. 3D24

CKFE

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIS: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

The "C" is (spelled)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OW nucleic - nucleic search, using sw model

Run on: February 7, 2006, 20:09:58 ; Search time 10535 Seconds
(without alignment)
11120.489 Million cell updates/sec

Title: US-10-817-591-16

Perfect score: 2061
Sequence: 1 atgagcgcctatcacgagccta.....atgaatggaagagtgctga 2061

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pac:*
7: gb_ph:*
8: gb_pr:*
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10: gb_scs:*
11: gb_by:*
12: gb_un:*
13: gb_vl:*
14: gb_hrg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 2 | 2061 | 100.0 | 2061 | 6 | AR640522 |
| 3 | 2061 | 100.0 | 2061 | 6 | AX441176 |
| 4 | 2061 | 100.0 | 2061 | 6 | AX467113 |
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| 6 | 1846.4 | 89.6 | 8791 | 13 | AY615798 |
| 7 | 1787 | 86.7 | 6329 | 6 | AX164584 |
| 8 | 1786 | 86.7 | 5360 | 6 | I06434 |
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| 22 | 1786 | 86.7 | 9401 | 6 | I81885 | I81885 Sequence 9 |
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ALIGNMENTS

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| LOCUS | CQ826998 | Sequence 1 from Patent WO2004048402. | | | |
| DEFINITION | CQ826998 | | | | |
| ACCESSION | CQ826998.1 | GI:49455655 | | | |
| VERSION | | | | | |
| KEYWORDS | | | | | |
| SOURCE | | | | | |
| ORGANISM | | | | | |
| synthetic construct | | | | | |
| synthetic construct | | | | | |
| other sequences; artificial sequences. | | | | | |
| REFERENCE | | | | | |
| 1 | Sallberg M. | | | | |
| AUTORS | | | | | |
| TITLE | | | | | |
| JOURNAL | | | | | |
| gene | | | | | |
| Patent: WO 2004048402-A 1 10-JUN-2004; | | | | | |
| TRIPEP AB (SE) | | | | | |
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| source | | | | | |
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| Best Local Similarity | 100.0% | Pred. No. 0; | | | |
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| Gaps | 0; | | | | |
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RESULT 2
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DEFINITION Sequence 16 from patent US 6858590.
ACCESSION AR640522
VERSION AR640522.1 GI:62775243
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2061)
AUTHORS Sallberg, M. and Hultgren, C.
TITLE Vaccines containing ribavirin and methods of use thereof
JOURNAL Patent: US 6858590-A 16 22-FEB-2005;
TRIPREP AB; Huddinge;
SEX;
FEATURES
source location/Qualifiers
1..2061

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2061; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
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LOCUS Sequence 16 from Patent WO0213855.
DEFINITION AX441176
ACCESSION AX441176
VERSION AX441176.1 GI:21665758
KEYWORDS
SOURCE
ORGANISM
other sequences; artificial sequences.
REFERENCE
1 Salberg, M. and Hultgren, C.
AUTHORS
TITLE
JOURNAL
Patent: WO 0213855-A 16 21-FEB-2002;
TRIPEP AB (SE)
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ORIGIN

Query Match 100.0%; Score 2061; DB 6; Length 2061;
Best Local Similarity 100.0%; Freq. No. 0;
Matches 2061; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DEFINITION Sequence 1 from Patent WO0214362.
ACCESSION AX467113
VERSION AX467113.1 GI:21900425
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Sallberg M.
TITLE A hepatitis C virus non-structural ns3/4a fusion gene
JOURNAL Patent: WO 0214362-A 1 21-FEB-2002;
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2061; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS HEC278830
DEFINITION Hepatitis C virus genomic RNA for polyprotein gene.
ACCESSION AJ278830
VERSION AJ278830.1 GI:9843676
KEYWORDS core protein; envelop protein 1; envelop protein 2; non-structural protein 2; non-structural protein 3; non-structural protein 4a; non-structural protein 4b; non-structural protein 5a; non-structural protein 5b; ORF1; ORF10; ORF2; ORF3; ORF4; ORF5; ORF6; ORF7; ORF8; ORF9; polyprotein.
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepcivirinae.
REFERENCE 1
AUTHORS Kumar,U., Tsuchii,T., Thomas,H.C. and Monjardino,J.
TITLE Sequence, expression and reconstruction of an HCV genome from a British isolate derived from a single blood donation
J. Viral Hepat. 7 (6), 459-465 (2000)
JOURNAL 1115058
PUBMED 2 (baaes 1 to 9610)
REFERENCE Kumar,U.
TITLE Direct Submission
JOURNAL Submitted (11-AUG-2000) Kumar U., Virology, GlaxoWellcome Research centre, Gunnels Wood Road, Stevenage, Hertfordshire, SG1 2NY,

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ACCESSION  AY615798
VERSION     AY615798.1 GI:48479029
KEYWORDS
SOURCE      Hepatitis C virus
ORGANISM    Hepatitis C virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
            Hepcivirus.
REFERENCE   1 (bases 1 to 8791)
AUTHORS     Branm,T.W., Kotchili,S., Polis,M. and Imamichi,T.
TITLE       Identification of mutations associated with interferon resistance
            in HCV and HIV co-infected patients
JOURNAL     Unpublished
AUTHORS     Branm,T.W., Kotchili,S., Polis,M. and Imamichi,T.
TITLE       Direct Submision
JOURNAL     Submitted (03-MAY-2004) LHR/CSP, SAIC-Frederick, Inc, Building 550,
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ORIGIN

Query Match

Best Local Similarity 93.5%; Score 1846.4; DB 13; Length 8791;

Matches 1925; Conservative 1; Mismatches 133; Indels 0; Gaps 0;

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LOCUS Sequence 48 from Patent EP 0318216.
DEFINITION 106434
ACCESSION 106434
VERSION 106434.1 GI:590311
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 5360)
AUTHORS Houghton,M., Choo,Q.-L. and Kuo,G.
TITLE Nandv diagnostics and vaccines
JOURNAL Patent: EP 0318216-A1 48 31-MAY-1989;
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DEFINITION Sequence 8 from Patent WO 8904669.
ACCESSION 109328
VERSION 109328.1 GI:587963
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 5360)
AUTHORS Houghton, M., Choo, Q.-K. and Kuo, G.
JOURNAL Patent: WO 8904669-A 8 01-JUN-1989;
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Query Match 86.7%; Score 1786; DB 6; Length 5360;
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| KEYWORDS | | | |
| SOURCE | Unknown. | | |
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| REFERENCE | Unclassified. | | |
| AUTHORS | 1 (bases 1 to 7310) | | |
| TITLE | Chien, D.Y. | | |
| JOURNAL | NANBV diagnostics and vaccines | | |
| FEATURES | Patent: US 6150087-A 74-21-NOV-2000; | | |
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ACCESSION 109331
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REFERENCE 1 (bases 1 to 7310)
AUTHORS Houghton,M., Choo,Q.-K. and Kuo,G.
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DEFINITION Hepatitis C virus polypeptide gene, partial cds.
ACCESSION M32084
VERSION M32084.1 GI:329875
KEYWORDS polypeptide.
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.
REFERENCE 1 (bases 1 to 7310)
AUTHORS Cho, Q.-L., Richman, K. and Han, J.
TITLE The nucleotide sequence of the Hepatitis C viral genome
JOURNAL Unpublished (1990)
COMMENT Original source text: Hepatitis C virus, cDNA to viral RNA, clones K9-1 through 15e, isolated from chimpanzee (individual 910) blood plasma.
Draft entry and printed sequence for (1) kindly submitted by M.Houghton, 22-FEB-1990. Chiron Corporation, 4560 Horton Street, Emeryville CA 94608.

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ORIGIN

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| | Homnidae; Homo. | | |
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| REFERENCE | Weiner,A.J., Steimer,K.S. and Houghton,M. | | |
| AUTHORS | HCV cultivation method in eucaryotic cells | | |
| TITLE | Patent: JP 2001314192-A 3 13-NOV-2001. | | |
| JOURNAL | CHIRON CORP | | |
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| | PI AY Y WEINER, KATHELYN S STEIMER, MICHAEL HOUGHTON PC | | |
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VERSION 108294.1 GI:588994
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ORGANISM Unknown.
REFERENCE 1 (bases 1 to 9185)
AUTHORS Houghton, M., Choo, Q., -L. and Kuo, G.
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Job time : 10539 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 7, 2006, 20:08:33 ; Search time 1260 Seconds
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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|----|--------|------|-------|----|---|
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| 21 | 1784.4 | 86.6 | 8316 | 2 | AAQ05955 Hepatitis AAd05955 Hepatitis |
| 22 | 1784.4 | 86.6 | 9185 | 2 | AAQ05956 Sense str AAd05956 Sense str |
| 23 | 1784.4 | 86.6 | 9185 | 2 | AAAT6737 Nucleotid AAd6737 Nucleotid |
| 24 | 1784.4 | 86.6 | 9185 | 2 | AAAT6737 Nucleotid AAd6737 Nucleotid |
| 25 | 1784.4 | 86.6 | 9400 | 2 | AAQ21744 Hepatitis AAd21744 Hepatitis |
| 26 | 1782.8 | 86.5 | 9185 | 2 | AAQ00459 Hepatitis AAd00459 Hepatitis |
| 27 | 1782.6 | 86.5 | 5300 | 1 | AAAN92097 Hepatitis AAd92097 Hepatitis |
| 28 | 1781.2 | 86.4 | 2058 | 6 | AAAD29795 HCV-1 NS3 AAd29795 HCV-1 NS3 |
| 29 | 1781.2 | 86.4 | 2058 | 6 | AAAD29795 HCV-1 NS3 AAd29795 HCV-1 NS3 |
| 30 | 1781.2 | 86.4 | 2058 | 10 | AAAD29795 HCV-1 NS3 AAd29795 HCV-1 NS3 |
| 31 | 1781.2 | 86.4 | 5360 | 11 | AAAN90327 Hepatitis AAd90327 Hepatitis |
| 32 | 1781.2 | 86.4 | 5360 | 11 | AAAN90327 Hepatitis AAd90327 Hepatitis |
| 33 | 1779.6 | 86.3 | 2058 | 6 | ABK15344 Hepatitis ABK15344 Hepatitis |
| 34 | 1779.6 | 86.3 | 2058 | 10 | ABK14410 DNA encod ABK14410 DNA encod |
| 35 | 1776.4 | 86.2 | 8316 | 12 | ADN35977 Hepatitis AAd35977 Hepatitis |
| 36 | 1774.8 | 86.1 | 12980 | 2 | AAAV59364 Hepatitis AAd59364 Hepatitis |
| 37 | 1774.8 | 86.1 | 12980 | 8 | AAAV59364 Hepatitis AAd59364 Hepatitis |
| 38 | 1774.8 | 86.1 | 16622 | 3 | AAAZ6212 Nucleotid AAd6212 Nucleotid |
| 39 | 1773.2 | 86.0 | 9379 | 2 | AAQ36209 Composite AAd36209 Composite |
| 40 | 1773.2 | 86.0 | 9646 | 2 | AAV59361 Hepatitis AAd59361 Hepatitis |
| 41 | 1773.2 | 86.0 | 9646 | 6 | ABK87285 CDNA encod ABK87285 CDNA encod |
| 42 | 1773.2 | 86.0 | 9646 | 8 | ACA62466 HCV H77 C AAd62466 HCV H77 C |
| 43 | 1773.2 | 86.0 | 12980 | 6 | ABK87286 Hepatitis ABK87286 Hepatitis |
| 44 | 1766.2 | 85.7 | 5961 | 14 | AAE62090 Replicati AAd62090 Replicati |
| 45 | 1766.2 | 85.7 | 11240 | 14 | AAE62089 Replicati AAd62089 Replicati |

ALIGNMENTS

| | |
|----------|--|
| RESULT 1 | |
| AD34500 | |
| ID | AD34500 standard, DNA, 2061 BP. |
| AC | AD34500; |
| XX | |
| DT | 16-JUL-2002 (first entry) |
| DE | Hepatitis C virus NS3/4A protein encoding DNA. |
| KW | Hepatitis C virus; HCV; NS3/4A protein; therapy; HCV infection; vaccine; |
| KW | viricide; gene; ds. |
| OS | Hepatitis C virus. |
| XX | |
| FT | Key |
| FT | CDS |
| FT | Location/Qualifiers |
| FT | 1..2061 |
| FT | /*tag= a |
| FT | /product= "HCV NS3/4A protein" |
| PN | WO200214362-A2. |
| PD | 21-FEB-2002. |
| XX | |
| PR | 15-AUG-2001; 2001WO-1B001774. |
| PR | 17-AUG-2000; 2000US-0225767P. |
| PR | 29-AUG-2000; 2000US-0229175P. |
| PR | 03-NOV-2000; 2000US-00705547. |
| XX | |
| PA | (TRIP-) TRIPER AB. |
| XX | |
| PI | Sallberg M; |
| XX | |
| DR | WPI; 2002-339446/37. |
| DR | P-PSDB; AAE21837. |
| PT | Novel hepatitis C virus NS3/4A peptide useful for diagnosing presence or |
| PT | absence of hepatitis C virus in a subject and for preparing a medicament |
| PT | for treating hepatitis C virus infection. |
| XX | |
| PS | Claim 1, Page 64-65; 90pp; English. |

XX The present invention relates to novel hepatitis C virus (HCV) NS3/4A
CC proteins and their corresponding polynucleotides. NS3/4A sequences are
CC useful for identifying the presence or absence of HCV in a subject. They are
CC useful for preparing a medicament used for treating or preventing HCV
CC infection. Sequences of the invention are also used as vaccines. The
CC present sequence is a DNA encoding HCV NS3/4A protein

XX Sequence 2061 BP; 427 A; 616 C; 571 G; 447 T; 0 U; 0 Other;

Query Match 100.0%; Score 2061; DB 6; Length 2061;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2061; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGGGCCATATACGGCCCTATGCCCCAGACAGAGGGGGCTTTGGAGATGATATACCC 60
DB 1 ATGGGGCCATATACGGCCCTATGCCCCAGACAGAGGGGGCTTTGGAGATGATATACCC 60
QY 61 ACCTTGACCGGCGGGACAAAACAGGTGAGGGGTTCAGATCGTCAACTGCT 120
DB 61 ACCTTGACCGGCGGGACAAAACAGGTGAGGGGTTCAGATCGTCAACTGCT 120
QY 121 GCCCAGACTTTCTTGGAACACTGCAATTAACGGGGTGTGTTGACCTGTTCAATGAGCC 180
DB 121 GCCCAGACTTTCTTGGAACACTGCAATTAACGGGGTGTGTTGACCTGTTCAATGAGCC 180
QY 181 GGAACAAGGACCATGGCGTCACTTAAGGGTCCCTGTTATCAGATGTACCAATGTGAC 240
DB 181 GGAACAAGGACCATGGCGTCACTTAAGGGTCCCTGTTATCAGATGTACCAATGTGAC 240
QY 241 CAAGACCTGTAGCTGAGCCCGCTCCCAAGGTGCCCCGCTCATTAACAACATGACTTGC 300
DB 241 CAAGACCTGTAGCTGAGCCCGCTCCCAAGGTGCCCCGCTCATTAACAACATGACTTGC 300
QY 301 GGGCTCTGGGACCTTTACTGTGTACAGAGGACAGCCGATGTCAATTCCTGTGCGGAGCG 360
DB 301 GGGCTCTGGGACCTTTACTGTGTGTACAGAGGACAGCCGATGTCAATTCCTGTGCGGAGCG 360
QY 361 GGTGATGGAGGGGACCGCTTGTCGCCCGGCGCTATCTTATCTTGAAGGCTCTCTCG 420
DB 361 GGTGATGGAGGGGACCGCTTGTCGCCCGGCGCTATCTTATCTTGAAGGCTCTCTCG 420
QY 421 GGAGGCGCTCTGTGTGCCCGCAGAGACATGCGTATGAGCATATTCAGAGCCCGGATATGC 480
DB 421 GGAGGCGCTCTGTGTGCCCGCAGAGACATGCGTATGAGCATATTCAGAGCCCGGATATGC 480
QY 481 ACCCGTGAAGTGGCTTAAGCGGTGACCTTCATCCCGTGAAGAGCTTGAAGACCAACCATG 540
DB 481 ACCCGTGAAGTGGCTTAAGCGGTGACCTTCATCCCGTGAAGAGCTTGAAGACCAACCATG 540
QY 541 AGGTCCCGGGTGTCTCAAGCAACTCTGCCACAGAGTGCCCCAGAGCTTACCAAGTG 600
DB 541 AGGTCCCGGGTGTCTCAAGCAACTCTGCCACAGAGTGCCCCAGAGCTTACCAAGTG 600
QY 601 GCCCAGCTTGATGCTCCACCGGAGCGGTAAAGACCAAGGTCCCGGCGCATACGCA 660
DB 601 GCCCAGCTTGATGCTCCACCGGAGCGGTAAAGACCAAGGTCCCGGCGCATACGCA 660
QY 661 GCTCAGGGCTAAGAGTGTGTGTCAACCCCTCGTGTGCAACAATGGGCTTTGGT 720
DB 661 GCTCAGGGCTAAGAGTGTGTGTCAACCCCTCGTGTGCAACAATGGGCTTTGGT 720
QY 721 GCTTACATGTCAAGGCGCATGGGATTTGATTCCTAATCAGATGAGGAGTGAAGCAAT 780
DB 721 GCTTACATGTCAAGGCGCATGGGATTTGATTCCTAATCAGATGAGGAGTGAAGCAAT 780
QY 781 ACTACTGAGAGCCGATCACTGATTCACACTACGGAAGTTCCTTCCGACGCGGGTGT 840
DB 781 ACTACTGAGAGCCGATCACTGATTCACACTACGGAAGTTCCTTCCGACGCGGGTGT 840
QY 841 TCAGGGGGTGTATTATGATTAATTTGTGACGAGTGCACCTCCAGATGCAACATCC 900
DB 841 TCAGGGGGTGTATTATGATTAATTTGTGACGAGTGCACCTCCAGATGCAACATCC 900

QY 901 ATCTTGGGCAATTGGCACTGTCTTGAACCAAGCAGAGACCGCGGGGCGAGACTGACTGNG 960
DB 901 ATCTTGGGCAATTGGCACTGTCTTGAACCAAGCAGAGACCGCGGGGCGAGACTGACTGNG 960
QY 961 CTGCGCACCGTACCCCTCCGGGCTCCGTCACTGTGCCCATCTTAACATGAGAGGTT 1020
DB 961 CTGCGCACCGTACCCCTCCGGGCTCCGTCACTGTGCCCATCTTAACATGAGAGGTT 1020
QY 1021 GCTCTGTCCATCAACCGGAGAGATCCCTTTTATGGCAAGGCTAATCCCTTAAACAAAT 1080
DB 1021 GCTCTGTCCATCAACCGGAGAGATCCCTTTTATGGCAAGGCTAATCCCTTAAACAAAT 1080
QY 1081 AAGGGGGGAGACATCTCATCTTCTGCCACTCAAGAAAGTGTGCGACGAGCTCCCGCA 1140
DB 1081 AAGGGGGGAGACATCTCATCTTCTGCCACTCAAGAAAGTGTGCGACGAGCTCCCGCA 1140
QY 1141 AAACCTGTGCGGTTGGGCGTCAATGCGGTGCTTACCTACCGGCGCTTGAATGTCTCCGTC 1200
DB 1141 AAACCTGTGCGGTTGGGCGTCAATGCGGTGCTTACCTACCGGCGCTTGAATGTCTCCGTC 1200
QY 1201 ATCCGACCAAGTGTGACGTTGTCTGTGTGCACTGACGCGCTCATGACCGGCTTTACC 1260
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DB 1261 GGCAGCTTGAATTGCGGTATGACTGCAACAGTGTGTGTCAACCCAGACAGTCACTTCAAGC 1320
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DB 1321 CTGACCCCTACCTTACCATTTGAGCAATCAAGCTTCCCGAGAGTCTGTCTCCGATCT 1380
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DB 1381 CAACGTGGGGTGAAGACCTGGAGAGGAGGACCAAGGACATCTACAGATTTGTGCAACGGGG 1440
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DB 1441 GAGCGTCTTCTGGGATGTTTGACTGTCTGTCTGTGCGAGTGTGTATGACCGGGTGTGT 1500
QY 1501 GCTTGTATGAGCTTATGAGCCCGCGCAGACCAAGTTAGGCTTACGAGCATATCAATGAACACC 1560
DB 1501 GCTTGTATGAGCTTATGAGCCCGCGCAGACCAAGTTAGGCTTACGAGCATATCAATGAACACC 1560
QY 1561 CCGGACCTTCCCGTGTGCAAGACCACTTGAATTTGGAGGGGCTTTACGGGCTCTC 1620
DB 1561 CCGGACCTTCCCGTGTGCAAGACCACTTGAATTTGGAGGGGCTTTACGGGCTCTC 1620
QY 1621 ACCCATATGAGCGCCCACTTCTATCCAGACCAAGAGTGGGAAAACCTTCCCTAT 1680
DB 1621 ACCCATATGAGCGCCCACTTCTATCCAGACCAAGAGTGGGAAAACCTTCCCTAT 1680
QY 1681 CTGTAGCGTACCAAGCAACCGTGTGCGCTAGAGCTCAAGCCCTTCCCGTGTGGAGAC 1740
DB 1681 CTGTAGCGTACCAAGCAACCGTGTGCGCTAGAGCTCAAGCCCTTCCCGTGTGGAGAC 1740
QY 1741 CAGATGTGAAGTGTGTTAATCCGTCTCAAGCCCACTTCCATGAGGCGCAACACTCTGCTA 1800
DB 1741 CAGATGTGAAGTGTGTTAATCCGTCTCAAGCCCACTTCCATGAGGCGCAACACTCTGCTA 1800
QY 1801 TATAGACTGGGCGCTGTCCAGAAATGAAGTCAACCTTGACGCAACCCAGTCAACAAATATATC 1860
DB 1801 TATAGACTGGGCGCTGTCCAGAAATGAAGTCAACCTTGACGCAACCCAGTCAACAAATATATC 1860
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DB 1861 ATGACATATATGTCCGCTGACCTGAGAGTGTGTACGAGTACTGTGGTGTGTGGCGGAC 1920
QY 1921 GTTCTGGCTGCTTTTGGCGCGGCTTATGCTTATCAAGAGTCTGTGGTGTCTTGGCTAGG 1980
DB 1921 GTTCTGGCTGCTTTTGGCGCGGCTTATGCTTATCAAGAGTCTGTGGTGTCTTGGCTAGG 1980


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Db 1141 AAACGTGTCGCGTGGCGCTCAATGCGGCTTAACCGCGGCTTGATGTCGCTC 1200
Qy 1201 ATCCGACCAAGTGTGACCTTGTCCGTGCGCAACGAGCCCTCAATGACCGGCTTTAC 1260
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Qy 1321 CTTTGACCTTACCTTCAACATGAGACATCAGCTTCCCGAGATGCTGTCCCGTACT 1380
Db 1321 CTTTGACCTTACCTTCAACATGAGACATCAGCTTCCCGAGATGCTGTCCCGTACT 1380
Qy 1381 CAACGTCGGGGTGTGAGCTGGCAGAGGGAGCCAGAGATTTAAGATTTGTGACCCGGG 1440
Db 1381 CAACGTCGGGGTGTGAGCTGGCAGAGGGAGCCAGAGATTTAAGATTTGTGACCCGGG 1440
Qy 1441 GAGCGTCTTCTGCGCATGTTTGACTGTCTGTCTCTGCGAGTGTATGACCGGGTGT 1500
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Qy 1501 GCTTGGTATGAGCTTACGCCCCCGAGACCAAGTAAAGCTTACGAGCATATGAACACC 1560
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Db 1681 CTGTGATGCTTACCAAGCCACCGTGTGCTTGAAGTCAAGCCCTTCCCGTGTGGAGC 1740
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Db 1741 CAGATGTGAGAGTGTGATCCGTCTCAAGCCCAACCTTCATGAGGCAACCTCTGCTA 1800
Qy 1801 TATAGACTGGGCGCTGTCCAGATGAGTCAACCTTGAACCCAGTCAACCAATATATC 1860
Db 1801 TATAGACTGGGCGCTGTCCAGATGAGTCAACCTTGAACCCAGTCAACCAATATATC 1860
Qy 1861 ATGACATGTATGTCCGCTGACCTGAGAGTGTCTACGAGTAACTTGGTGTGGCGC 1920
Db 1861 ATGACATGTATGTCCGCTGACCTGAGAGTGTCTACGAGTAACTTGGTGTGGCGC 1920
Qy 1921 GTTCTGGGCTGCTTTGGCGCGGATGCTTATCCACAGGCTGTGGTGTATAGTATAG 1980
Db 1921 GTTCTGGGCTGCTTTGGCGCGGATGCTTATCCACAGGCTGTGGTGTATAGTATAG 1980
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Db 1981 ATTGTCTTGTCCGGAAGCCGCAATCATACCGACAGGGAAGTCTTACCGGGAGTTC 2040
Qy 2041 GATGAATGGAAGAGTGTGA 2061
Db 2041 GATGAATGGAAGAGTGTGA 2061
```

```
RESULT 3
AAd60868 standard; DNA; 2061 BP.
XX
AC AAd60868;
XX
DT 15-JAN-2004 (first entry)
XX
DE Hepatitis C virus NS3/4A DNA.
XX
```

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1
```

```
KW Ribavirin; vaccine; immune response; infection; therapy; immunostimulant;
KM virucide; ds.
XX
OS Hepatitis C virus.
XX
FH Key Location/Qualifiers
FT 1..2061
FT /tag= a
FT /product= "Hepatitis C virus protein"
XX
PN US2002136740-A1.
XX
PD 26-SEP-2002.
XX
PF 15-AUG-2001; 2001US-00929955.
XX
PR 17-AUG-2000; 2000US-0225767P.
PR 29-AUG-2000; 2000US-0229175P.
XX
PA (SALL/) SALLBERG M.
PA (HULT/) HULTGREN C.
XX
PI Sallberg M, Hultgren C;
XX
DR WPI; 2003-764978/72.
DR P-PsDB; ABW00351.
XX
PT Vaccine compositions for treating and preventing disease, preferably
PT hepatitis C virus infection, comprises ribavirin and antigen that has
PT epitope present in hepatitis C virus.
XX
PS Claim 1, Page 60-61; Opp; English.
XX
CC The invention relates to a composition comprising ribavirin and an
CC antigen, where the antigen is derived from a hepatitis virus. The vaccine
CC is useful in enhancing the immune response to a hepatitis C antigen where
CC the composition is delivered to an animal identified as requiring an
CC enhanced immune response. The vaccine is useful in the treatment and
CC prevention of hepatitis C infection. The present sequence is Hepatitis C
CC virus NS3/4A DNA
XX
SQ Sequence 2061 BP; 427 A; 616 C; 571 G; 447 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 2061; DB 10; Length 2061;
Beef Local Similarity 100.0%; Pred. No. 0;
Matches 2061; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGGCGCTTATCAAGGCTATGCCCCAGACAGACAGAGGCGCTTTGGAGTGAATATCACC 60
Db 1 ATGGCGCTTATCAAGGCTATGCCCCAGACAGACAGAGGCGCTTTGGAGTGAATATCACC 60
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Qy 121 GCCGAGCTTCTTGGCAACCTGATTTAAGGAGGTGTGTGAGTGTCTTACCATGAGGC 180
Db 121 GCCGAGCTTCTTGGCAACCTGATTTAAGGAGGTGTGTGAGTGTCTTACCATGAGGC 180
Qy 181 GGAACAGAGACATTTGCGTACCTAAGGCTCTGTTATTCAGATGTATACCAATGTGAGC 240
Db 181 GGAACAGAGACATTTGCGTACCTAAGGCTCTGTTATTCAGATGTATACCAATGTGAGC 240
Qy 241 CAAGACTCTGTAGGTGCGCGGCTCCCAAGGTGCGCGTCAATTAACACCATGACTTGC 300
Db 241 CAAGACTCTGTAGGTGCGCGGCTCCCAAGGTGCGCGTCAATTAACACCATGACTTGC 300
Qy 301 GGCCTCTGGAGACTTTACTGTGTGACAGAGGAGCGCGAGTGCATTCTGTGCGCGAGCG 360
Db 301 GGCCTCTGGAGACTTTACTGTGTGACAGAGGAGCGCGAGTGCATTCTGTGCGCGAGCG 360
Qy 361 GGTGATGCGAGGGGAGGCTGTTTGGCCCGGCTTATCTTACTTGAAGGCTCTCG 420
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Db 361 GGTGATGGCAGGGGAGCGCTGCTTTCGCCCGGCGCATCTTACTTGAAGAGCTCTCG 420
 Qy 421 GGAAGCCCTCTGCTGTGCCCCGAGAGATGCGGTAGGATATTAGAGCCCGGTATGC 480
 Db 421 GGAAGCCCTCTGCTGTGCCCCGAGAGATGCGGTAGGATATTAGAGCCCGGTATGC 480
 Qy 481 ACCCGTGAAGTGGCTAAGCGCGTGAATTCATCCCGTGAAGAGCTTGAAGACATC 540
 Db 481 ACCCGTGAAGTGGCTAAGCGCGTGAATTCATCCCGTGAAGAGCTTGAAGACATC 540
 Qy 541 AGGTCCCGGTGTCTCAGACAACTCTCCACAGAGTCCCGAGACTACCAAGT 600
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 Db 661 GCTCAGGCTCAAGAGTGTGCTCAACCCCTCGTTGCTGCAACAATGAGCTTTGGT 720
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 Db 721 GCTTACATGTCCAAAGGCCCATGGAATTGATCTTAAATCAGAGCTGGGTGAGCAAT 780
 Qy 781 ACTACTGGCAGGCCCATGCACTTTCACCTACCGCAAGTCTCTGGCGACCGCGGTGT 840
 Db 781 ACTACTGGCAGGCCCATGCACTTTCACCTACCGCAAGTCTCTGGCGACCGCGGTGT 840
 Qy 841 TCAGGGGGTGTATTAGACATAATTAATTGTGACGAGTGCCTCCAGGATGCAATCC 900
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 Db 1321 CTTGACCTTCACTTCACTTGAACATCAGCTTCCCGAGAGTGTCTCCGTA 1380
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Qy 1501 GCTTGTATGAGCTTACGCCCGCAGAGACCAAGTTAGGCTTACGAGCATATGAAAC 1560
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 Db 1621 ACCCATATGAGAGCCCATCTTCTATCCAGACAAAGCAGAGTGGGAAAACTTCCCTAT 1680
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 Db 1741 CAGATGTGAAGTGTCTGATCCGTCTCAAGCCCATCTTCATGGGCCCAACCTCTGCTA 1800
 Qy 1801 TATAGACTGGGCGCTGTCCAGATGAAGTCACTTGAAGCAGCAGTCAACCAAGTATATC 1860
 Db 1801 TATAGACTGGGCGCTGTCCAGATGAAGTCACTTGAAGCAGCAGTCAACCAAGTATATC 1860
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 Db 1861 ATGACATGATGTGGGCTGACCTGAGAGTGTGACAGAGTACTGGGTGCTGTTGGCGGC 1920
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 Db 1921 GTTCTGCTGTCTTTGGCGCGATGATGCTTATCCAGAGCTGGGTGCTATGAGTAG 1980
 Qy 1981 ATTGTCTTGTCCGGAAGCCGCAATCATATCCGACAGGGAAGTCTTACCGGAGTTC 2040
 Db 1981 ATTGTCTTGTCCGGAAGCCGCAATCATATCCGACAGGGAAGTCTTACCGGAGTTC 2040
 Qy 2041 GATGAATGGAAGAGTGTGA 2061
 Db 2041 GATGAATGGAAGAGTGTGA 2061

RESULT 4
 ADG47658 standard; DNA; 2061 BP.
 ID ADG47658;
 AC ADG47658;
 XX
 DT 11-MAR-2004 (first entry)
 XX
 DE HCV NS3/4A domain DNA.
 XX
 KW ds; gene; immunogen; hepatitis C virus; HCV infection; vaccine.
 XX
 OS Hepatitis C virus.
 FT Key Location/Qualifiers
 FT CDS 1..2061
 FT /tag= a
 FT /product= "NS3/4A domain"
 PN US2003206919-A1.
 XX
 PD 06-NOV-2003.
 XX
 PF 26-NOV-2002; 2002US-00307047.
 XX
 PR 17-AUG-2000; 2000US-0225767P.
 PR 29-AUG-2000; 2000US-0228175P.
 PR 15-AUG-2001; 2001US-00929955.
 PR 15-AUG-2001; 2001US-00930591.
 XX
 PA (SALL/) SALLBERG M.

XX Salberg M;
PI
XX
DR MPI: 2004-051480/05.
DR P-PSDB; ADG47659.

PT New purified or isolated nucleic acid useful for enhancing an immune
PT response to a hepatitis C antigen comprises specific nucleotide sequences
PT and the amino acid sequences.

XX
PS Example 1; SEQ ID NO 1; 83bp; English.

XX The invention relates to a purified or isolated nucleic acid. The
XX peptides are useful as immunogens for the treatment and prevention of
CC hepatitis C virus (HCV) infection, in vaccine and immunogen compositions.
CC The nucleic acid and the peptide enhance an immune response to a
CC hepatitis C antigen and are potent immunogens. The present sequence is
CC used in the exemplification of the invention.

XX
SQ Sequence 2061 BP; 427 A; 616 C; 571 G; 447 T; 0 U; 0 Other;

Query Match 100.0%; Score 2061; DB 12; Length 2061;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2061; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGGCGCTATACGCGCTATGCGCGAGACAAAGGGGCTTTGGAGATGCAATATCAC 60
DB 1 ATGGGCGCTATACGCGCTATGCGCGAGACAAAGGGGCTTTGGAGATGCAATATCAC 60
QY 61 AGCTTGACCGGCGGAGACAAAACAGGTGAGGTGAGGTTCAAGTCGTCAACTGCT 120
DB 61 AGCTTGACCGGCGGAGACAAAACAGGTGAGGTGAGGTTCAAGTCGTCAACTGCT 120
QY 121 GCCCGACCTTTTGGCAACCTGATTAACGGGGTGTGTGACCTGTCAACATGAGGC 180
DB 121 GCCCGACCTTTTGGCAACCTGATTAACGGGGTGTGTGACCTGTCAACATGAGGC 180
QY 181 GGAACAGGACCATTTGCGTCACTAAGGTCCTGTTATCCAGATGACACCAATGTGAC 240
DB 181 GGAACAGGACCATTTGCGTCACTAAGGTCCTGTTATCCAGATGACACCAATGTGAC 240
QY 241 CAAGACCTTGATGAGCTGCGCGCTCCCAAGGTGCCGCTCATTAACACCATGACCTTGC 300
DB 241 CAAGACCTTGATGAGCTGCGCGCTCCCAAGGTGCCGCTCATTAACACCATGACCTTGC 300
QY 301 GCGTCTCGGACCTTTAAGCTGTGACAGAGGACGCGGATGATTCCTGTGCGCGAGCG 360
DB 301 GCGTCTCGGACCTTTAAGCTGTGACAGAGGACGCGGATGATTCCTGTGCGCGAGCG 360
QY 361 GGTGATGAGGAGGAGCGCTGCTTTGCGCGGCTATCTTTAATTGAAAGGCTCTCG 420
DB 361 GGTGATGAGGAGGAGCGCTGCTTTGCGCGGCTATCTTTAATTGAAAGGCTCTCG 420
QY 421 GGAAGGCGCTCTGCTGTGCGCGAGAGACATGCGTATGAGCATATTCAGAGCGCGATATGC 480
DB 421 GGAAGGCGCTCTGCTGTGCGCGAGAGACATGCGTATGAGCATATTCAGAGCGCGATATGC 480
QY 481 ACCCGTGAAGTGAAGCGCGGTGACCTTCAATCCCGTGAAGAGCTTAAAGCAACCATG 540
DB 481 ACCCGTGAAGTGAAGCGCGGTGACCTTCAATCCCGTGAAGAGCTTAAAGCAACCATG 540
QY 541 AGGTCCCGGCTGTTCTCAGACAACTCTCCCAACGAGAGTGCCTCAGAGCTAACCAAGT 600
DB 541 AGGTCCCGGCTGTTCTCAGACAACTCTCCCAACGAGAGTGCCTCAGAGCTAACCAAGT 600
QY 601 GCCCACTTGATGCTCCCAACGAGAGGTGAAGAGCAACCAAGTCCCGCGCATATGCA 660
DB 601 GCCCACTTGATGCTCCCAACGAGAGGTGAAGAGCAACCAAGTCCCGCGCATATGCA 660
QY 661 GCTCAAGGCTTAAAGGTGCTGTGCTCAACCCCTCGTGTGCAACAATGAGGCTTTGGT 720
DB 661 GCTCAAGGCTTAAAGGTGCTGTGCTCAACCCCTCGTGTGCAACAATGAGGCTTTGGT 720

QY 721 GCTTACATGATCCAAAGGCCCATAGGATGATCTTAAATCAGAGCTGAGGTGAGCAAT 780
DB 721 GCTTACATGATCCAAAGGCCCATAGGATGATCTTAAATCAGAGCTGAGGTGAGCAAT 780
QY 781 ACTACTGAGAGCGGATCAAGTATTCACCTTACGCGAAGTTCTTGGCCGAGCGGGTGT 840
DB 781 ACTACTGAGAGCGGATCAAGTATTCACCTTACGCGAAGTTCTTGGCCGAGCGGGTGT 840
QY 841 TCAGGGGGTGTATGATATTAATTTGTGACGAGTGCATCCAGAGATGCAATCC 900
DB 841 TCAGGGGGTGTATGATATTAATTTGTGACGAGTGCATCCAGAGATGCAATCC 900
QY 901 ATCTTGAGGCAATTTGACATGCTCTTGACCAAGAGAGACCGCGGGGAGAGCTGAG 960
DB 901 ATCTTGAGGCAATTTGACATGCTCTTGACCAAGAGAGACCGCGGGGAGAGCTGAG 960
QY 961 CTGCGCACCGCTACCCCTCCGGGCTCCGTCACTGTGCCCATCTTAACATCAGAGAGGTT 1020
DB 961 CTGCGCACCGCTACCCCTCCGGGCTCCGTCACTGTGCCCATCTTAACATCAGAGAGGTT 1020
QY 1021 GCTCTGTCACTACCGGAGAGATCCCTTTATAGGCAAGGCTATCCCTTGAAGCAAT 1080
DB 1021 GCTCTGTCACTACCGGAGAGATCCCTTTATAGGCAAGGCTATCCCTTGAAGCAAT 1080
QY 1081 AAGGGGGGAGACATCTCATCTTCTGCCACTCAAGAAAGAGTGCAGAGCTCGCGCA 1140
DB 1081 AAGGGGGGAGACATCTCATCTTCTGCCACTCAAGAAAGAGTGCAGAGCTCGCGCA 1140
QY 1141 AAACGTGTGCGTGTGGGCGTCAATGCGGCTTACCTACCGGCGCTTGAATGTCCGT 1200
DB 1141 AAACGTGTGCGTGTGGGCGTCAATGCGGCTTACCTACCGGCGCTTGAATGTCCGT 1200
QY 1201 ATCCGACCAAGTGTGAGTGTGTGCGTGTGCAATGACGCGCTCATGACCGGCTTTACC 1260
DB 1201 ATCCGACCAAGTGTGAGTGTGTGCGTGTGCAATGACGCGCTCATGACCGGCTTTACC 1260
QY 1261 GCGCATCTTGATCGGTATGACTGCAACAGTGTGTACCCAGACAGTGCACCTTAC 1320
DB 1261 GCGCATCTTGATCGGTATGACTGCAACAGTGTGTACCCAGACAGTGCACCTTAC 1320
QY 1321 CTGACCTTACCTTACCAATGAGCAATACGCTTCCCGAGATGCTGTCTCCGTACT 1380
DB 1321 CTGACCTTACCTTACCAATGAGCAATACGCTTCCCGAGATGCTGTCTCCGTACT 1380
QY 1381 CAAGGTGGGGTGAAGACGCGAGAGGAGGAGGAGCATCTAAGATTTGTGCAACGGGG 1440
DB 1381 CAAGGTGGGGTGAAGACGCGAGAGGAGGAGGAGCATCTAAGATTTGTGCAACGGGG 1440
QY 1441 GAGCGTCTTCTGCGATGTTTGAATGCTGTCTCTGCGAGTGTGATGACCGGGTGT 1500
DB 1441 GAGCGTCTTCTGCGATGTTTGAATGCTGTCTCTGCGAGTGTGATGACCGGGTGT 1500
QY 1501 GCTTGTATGACTTACCGCGCGAGACCAAGTTAGGCTTACGAGCATATGAAACACC 1560
DB 1501 GCTTGTATGACTTACCGCGCGAGACCAAGTTAGGCTTACGAGCATATGAAACACC 1560
QY 1561 CCGGACCTTCCCGTGTGCAAGACATCTGAAATTTTGGAGAGGGGCTTTACGGGCTTC 1620
DB 1561 CCGGACCTTCCCGTGTGCAAGACATCTGAAATTTTGGAGAGGGGCTTTACGGGCTTC 1620
QY 1621 ACCCACTAGAGCGCCACTTCTATCCAGCAAAAGAGAGTGGGAAAACTTCCCTAT 1680
DB 1621 ACCCACTAGAGCGCCACTTCTATCCAGCAAAAGAGAGTGGGAAAACTTCCCTAT 1680
QY 1681 CTGTAAGGTACCAAGCAACGCTGTGCTAGAGCTCAAGCCCTTCCCGCTGTGAGAC 1740
DB 1681 CTGTAAGGTACCAAGCAACGCTGTGCTAGAGCTCAAGCCCTTCCCGCTGTGAGAC 1740
QY 1741 CAGATGGAAGTGTGATCCGTCTCAAGCCCAACCTTCAGAGGAGCAACACTCTGTGA 1800
DB 1741 CAGATGGAAGTGTGATCCGTCTCAAGCCCAACCTTCAGAGGAGCAACACTCTGTGA 1800
QY 1801 TATAGACTGGGCGTGTCCAGATGAGTCACTGACGCAACCAAGTCAATATATC 1860

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Db 1801 TATGACGGGGGGCTGTCCAGATGAGTCAACCTCGAGCACCAGTCAACCAAGATATTC 1860
Qy 1861 ATGACATATATGTGCGGCTGACCTGAGAGTCTGTCAAGATGCTGGGTCTGTTGGCGGC 1920
Db 1861 ATGACATATATGTGCGGCTGACCTGAGAGTCTGTCAAGATGCTGGGTCTGTTGGCGGC 1920
Qy 1921 GTTCTGCTGCTTTGGCGCGGATTTGCTATCCACAGGCTGGGTGATAGTAGTAGG 1980
Db 1921 GTTCTGCTGCTTTGGCGCGGATTTGCTATCCACAGGCTGGGTGATAGTAGTAGG 1980
Qy 1981 ATTGTCTTGTCCGGAAGCCCGCAATCATATCCGACAGGAAAGTCTCTACCGGAGTTC 2040
Db 1981 ATTGTCTTGTCCGGAAGCCCGCAATCATATCCGACAGGAAAGTCTCTACCGGAGTTC 2040
Qy 2041 GATGAAATGGAAGAGTCTGA 2061
Db 2041 GATGAAATGGAAGAGTCTGA 2061

RESULT 5
AAF83669
ID AAF83669 standard; DNA; 6299 BP.
AC
AAAF83669;
XX
DT 23-JUN-2001 (first entry)
XX
DE HCV NS34A ORF comprising PCMV-NS34A nucleic acid sequence.
XX
KW HCV; mutant; non-structural protein; NS; hepatitis C virus; mutation;
KM catalytic domain; NS3; NS4; NS5; antiviral; vaccine; immunostimulant;
KM immunotherapy; NS34A; de.
XX
OS Synthetic.
OS Hepatitis C virus.
XX
FH Key Location/Qualifiers
FT CDS 1990..4050
FT /tag= a
FT /product= "NS34A"
XX
XX MO20038360-A2.
XX
XX 31-MAY-2001.
XX
XX 22-NOV-2000; 2000MO-US032326.
XX
XX 24-NOV-1999; 99US-0167502P.
XX
XX (CHIR ) CHIRON CORP.
XX
XX Colt D, Medina-Selby A, Selby M, Houghton M;
XX
XX MPI; 2001-343948/36.
XX
XX P-PSDB; AAB62633.
XX
XX Mutant non-structural (NS) Hepatitis C virus (HCV) polypeptide, useful as
XX a vaccine against HCV, comprises a polypeptide having a mutation that
XX functionally disrupts the catalytic domain of NS3.
XX
XX Dieckhouse; Fig 9, 340pp; English.
XX
XX The invention relates to an isolated mutant non-structural (NS) Hepatitis
XX C virus (HCV) polypeptide, comprising a polypeptide having a mutation in
XX the catalytic domain of NS3, where the mutation functionally disrupts the
XX catalytic domain. The NS mutant polypeptides can include NS3, NS4 (NS4a
XX and NS4b) NS5 (NS5a and NS5b) or portions thereof. The HCV polypeptide
XX and polynucleotide (preferably DNA or a plasmid) compositions can be used
XX in vaccines against HCV and as diagnostics. The antibodies raised against
XX these polypeptides can also be used as diagnostics, or for passive
XX immunotherapy. The antibodies are also useful for isolating and
XX identifying HCV particles. The present sequence represents the nucleic
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CC acid sequence of the PCMV-NS34A comprising the ORF encoding a NS34A
CC polypeptide
xx
SQ Sequence 6299 BP, 1449 A; 1713 C; 1637 G; 1500 T; 0 U; 0 Other;
Query Match 86.7%; Score 1787; DB 4; Length 6299;
Best Local Similarity 91.7%; Pred. No. 0;
Matches 1889; Conservative 0; Mismatches 170; Indels 0; Gaps 0;
Qy 1 ATGGGCGCTTATCAGGCGCTATAGCCAGACAGAGGGGCTTTGGATGATATATCACC 60
Db 1990 ATGGGCGCCATCAGCGCCTTAGCGCCAGACAGAGGGGCTTCTAGGGTGAATATCACC 2049
Qy 61 AGCTTGACCGGCGGGGACAAAACAGGGTGAAGGGTGAAGTTACAGATGTCATCTGCT 120
Db 2050 AGCTTACTTGCGCGGGACAAAACAGGGTGAAGGGTGAAGTTACAGATGTCATCTGCT 2109
Qy 121 GCCCAGACTTTCTTGGCAACTGTCAATTAAAGGGGTGTGGACTGTCTACCATGAGCC 180
Db 2110 GCCCAAACTTCTTGGCAACGTGATCAATGGGGGTGTGCTGACTGTCTACCAAGGGCC 2169
Qy 181 GGAACAGAGACCATTTGGCTGACCTTAAGGGTCTGTATTCCAGATGTACCAATGTGAC 240
Db 2170 GGAACAGAGACCATTCGCTCAACCCAAAGGCTCTGTCAATGATGTATACCAATGTAGAC 2229
Qy 241 CAAGACCTGTAGAGCTGGCCCGCTCCCAAGGTGCGGCTCATTAACCAATGACTTGC 300
Db 2230 CAAGACCTTGTGGGCTGGCCCGCTTCCGAAGGTACCCGCTCATTAACCAATGACTTGC 2289
Qy 301 GGCTCTCTGGAACCTTTACCTGTGTCAAGAGGACCGCGATGTCAATTCGTGTGGCGGACGG 360
Db 2290 GGCTCTCTGGAACCTTTACCTGTGTCAAGAGGACCGCGATGTCAATTCGTGTGGCGGACGG 2349
Qy 361 GGTGATGACAGGGGACGCTTGTGCTTCCCGGCTTATCTTACTTGAAGGCTTCTGC 420
Db 2350 GGTGATGACAGGGGACGCTTGTGCTTCCCGGCTTATCTTGAAGGCTTCTGC 2409
Qy 421 GGAAGCCCTCTGCTGTGTCGCGCGGACGATGCGGTGATTCAGAGGCGCGGTATGC 480
Db 2410 GGAAGCCCTCTGCTGTGTCGCGCGGACGATGCGGTGATTCAGAGGCGCGGTATGC 2469
Qy 481 ACCGCTGAGTGTGCTTAAGCGGTGTGACTTCAATCCCGGTAGAGAGCTTAGAGCAACATG 540
Db 2470 ACCGCTGAGTGTGCTTAAGCGGTGTGACTTCAATCCCGGTAGAGAGCTTAGAGCAACATG 2529
Qy 541 AGGTCCCGGTGTGCTTCAAGCAATCTTCTCCCAACGAGTGTGCGGCAAGTCAAGTG 600
Db 2530 AGGTCCCGGTGTGCTTCAAGCAATCTTCTCCCAACGAGTGTGCGGCAAGTCAAGTG 2589
Qy 601 GCCGACCTGCAATGCTCCCAACGGGAGGGTAAAGACCAAGGTCCGGGCGCATATACGA 660
Db 2590 GCTACCTTCATGCTCCCAACGGGAGCGGCAAAAGACCAAGGTCCGGGCGCATATACGA 2649
Qy 661 GCTCAGGCTTCAAGAGTGTGCTCAACCCCTCTGTTGTGTCGAACATAGGGCTTTGGT 720
Db 2650 GCTCAGGCTTCAAGAGTGTGCTCAACCCCTCTGTTGTGTCGAACATAGGGCTTTGGT 2709
Qy 721 GCTTACATGTCGAAGGCCCATAGGATGATCTTAAATCAGAGACTGGGGTGAAGCAATT 780
Db 2710 GCTTACATGTCGAAGGCCCATAGGATGATCTTAAATCAGAGACTGGGGTGAAGCAATT 2769
Qy 781 ACTACTGGCAGCCCGATACAGTATTCGACCTTACCGGCAAGTTCTTGGACGAGGGGGTGT 840
Db 2770 ACTACTGGCAGCCCGATACAGTATTCGACCTTACCGGCAAGTTCTTGGACGAGGGGGTGT 2829
Qy 841 TCAGGGGGTGTGTTATGACATATATTTGTGACAGTGTCCATCCAGATGCAATGCC 900
Db 2830 TCAGGGGGTGTGTTATGACATATATTTGTGACAGTGTCCATCCAGATGCAATGCC 2889
Qy 901 ATCTTGGGCAATTTGGCACTGTCTTGAACCAAGAGACCGGGGGGCAAGTCACTGTG 960
Db 2890 ATCTTGGGCAATTTGGCACTGTCTTGAACCAAGAGACTGTGGGGGCAAGTCACTGTGTG 2949
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QY 961 CTGGCACCAGTACCCCTCCGGGCTCCGTCACGTGTCGCCCATCTTAACATGAGAGGTT 1020
DB 2950 CTGGCACCAGTACCCCTCCGGGCTCCGTCACGTGTCGCCCATCTTAACATGAGAGGTT 3009
QY 1021 GCTGTGTCACCTACCGAGAGATCCCTTTTATGCGAGGCTATTCCCTTTAGACAAAT 1080
DB 3010 GCTGTGTCACCGAGAGATCCCTTTTATGCGAGGCTATTCCCTTTAGACAAAT 3069
QY 1081 AAGGGGGGAGACATCTCATCTTTGCGCACTCAAGAGAAATGCGAGAGCTCCCGCA 1140
DB 3070 AAGGGGGGAGACATCTCATCTTTGCGCACTCAAGAGAAATGCGAGAGCTCCCGCA 3129
QY 1141 AACTGTGTGCGGCTGATGATGCGGCTTACTACCGGAGCTTGTATGTCGCTC 1200
DB 3130 AAGGTGTGCTATGCGGCTGATGATGCGGCTTACTACCGGAGCTTGTATGTCGCTC 3189
QY 1201 ATCCGACCAAGTGTGACGTTGTCGTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 1260
DB 3190 ATCCGACCAAGTGTGACGTTGTCGTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 3249
QY 1261 GCGGACTTGTGATTCGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320
DB 3250 GCGGACTTGTGATTCGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 3309
QY 1321 CTGACACCTTACCTTCACTTGAAGACATCAAGCTTCCCGAGATGCTGCTCCGCTACT 1380
DB 3310 CTGACACCTTACCTTCACTTGAAGACATCAAGCTTCCCGAGATGCTGCTCCGCTACT 3369
QY 1381 CAACGTCGGGGGTAGACCTGCGACAGAGGAAAGCAGAGATCTACAGATTTGTGACACCGGG 1440
DB 3370 CAACGTCGGGGGTAGACCTGCGACAGAGGAAAGCAGAGATCTACAGATTTGTGACACCGGG 3429
QY 1441 GAGCGCTCTTGTGCGATGTTTGAATCTGTCCTCTGTCGATGCTATGACCGCGGTGT 1500
DB 3430 GAGCGCTCTTGTGCGATGTTTGAATCTGTCCTCTGTCGATGCTATGACCGCGGTGT 3489
QY 1501 GCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
DB 3490 GCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3549
QY 1561 CCGGGACCTTCCCGTGTGCGCAAGACATCTTGAATTTTGGAGGCGCTTTTACGCGCTC 1620
DB 3550 CCGGGACCTTCCCGTGTGCGCAAGACATCTTGAATTTTGGAGGCGCTTTTACGCGCTC 3609
QY 1621 ACCCATATGAGCGCCCATCTTCTATTCGCGACAAAGACAGATGCGGAAAACTTCCCTAT 1680
DB 3610 ACCCATATGAGCGCCCATCTTCTATTCGCGACAAAGACAGATGCGGAAAACTTCCCTAT 3669
QY 1681 CTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740
DB 3670 CTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3729
QY 1741 CAGATGTGAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1800
DB 3730 CAGATGTGAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3789
QY 1801 TATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1860
DB 3790 TATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3849
QY 1861 ATGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1920
DB 3850 ATGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3909
QY 1921 GTTGTGCTGCTTTTGGCGCGATGATGATGATGATGATGATGATGATGATGATGATGAT 1980
DB 3910 GTTGTGCTGCTTTTGGCGCGATGATGATGATGATGATGATGATGATGATGATGATGAT 3969
QY 1981 ATTGTCTTGTCCGGAAGCGCGCAATCAATCCGAGAGAGAGAGAGAGAGAGAGAGAGAG 2040
DB 3970 ATTGTCTTGTCCGGAAGCGCGCAATCAATCCGAGAGAGAGAGAGAGAGAGAGAGAGAG 4029
QY 2041 GATGAATGGAAGAGTCT 2059

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DB 4030 GATGATGGAAGAGTCT 4048

RESULT 6
ID AAN92106 standard; DNA; 7310 BP.
XX
AC AAN92106;
XX
DT 09-SEP-2004 (revised)
DT 25-MAR-2003 (revised)
DT 02-MAR-1990 (first entry)
XX
DE Combined ORFs of the HCV cDNAs from clones K9-1 through 15e.
XX
KW Hepatitis C virus; HCV; non-A, non-B hepatitis; NANBH; ss.
OS Hepatitis C virus.
OS Unidentified.
XX
FH Key
FT CDS Location/Qualifiers
FT 3..7310
FT /*tag= a
XX
EP318216-A.
XX
PD 31-MAY-1989.
XX
PF 18-NOV-1988; 88BP-00310922.
XX
PR 18-NOV-1987; 87US-00122714.
PR 30-DEC-1987; 87US-00139886.
PR 26-FEB-1988; 88US-00161072.
PR 06-MAY-1988; 88US-00191263.
PR 26-OCT-1988; 88US-00263584.
PR 14-NOV-1988; 88US-00271450.
XX
PA (CHIR ) CHIRON CORP.
PA (CHIR ) CHIRON CORP.
XX
Houghton M, Choo QL, Kuo G;
XX
DR MPI: 1989-159274/22.
XX
DR P-PSDB; AAP92050.
XX
PT Purified hepatitis C virus - and associated nucleic acids and
PT polypeptide(s).
XX
PS Claim 3; Fig 47-1 - 47-8; 139pp; English.
XX
CC It is a double-stranded nucleotide sequence of the open reading frame
CC (ORF) (tag a) extending through clones K9-1 to 15e of hepatitis C virus
CC (HCV) cDNA. It can be used to make oligomeric DNA hybridisation probes to
CC detect the presence of HCV nucleic acids in samples. The polypeptide(s)
CC it encodes could be used as immunoassay reagents and vaccines and to
CC generate antibodies useful in diagnosis and passive immunotherapy for HCV
CC infection/non-A, non-B hepatitis. (Updated on 25-MAR-2003 to correct PR
CC field.) (Updated on 25-MAR-2003 to correct PI field.)
CC
CC Revised record issued on 09-SEP-2004 : Correction to keywords
XX
SQ Sequence 7310 BP; 1491 A; 2217 C; 2058 G; 1540 T; 0 U; 4 Other;
XX

Query Match 86.7%; Score 1786; DB 1; Length 7310;
Best Local Similarity 91.7%; Pred. No. 0;
Matches 1888; Conservative 0; Mismatches 170; Indels 0; Gaps 0;

QY 2 TGGCGCCCTATACCGGCTATGCGCGAGACAGAGGCGCTTTTGGATGCAATATCACCA 61
DB 1729 TGGCGCCCTATACCGGCTATGCGCGAGACAGAGGCGCTTCTTGGATGCAATATCACCA 1788
QY 62 GCTTACCGCGCGGAGCAAAAAACAGTGAAGGTGAGGTTGAGATCTGTCAACTGCTG 121

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Db 1789 GCTTAACTGCGCGGAGCAAAAACCAAGTGAAGGTGAGGTCCAGATTGTGTCAACTGCTGG 1848
 Qy 122 CCCAATCTTTCTTGGCAACTGCAATTAAGGGGTGTGTGAACTGTCTTCACTGAGCCG 181
 Db 1849 CCCAAACCTTCTCGCAAGTGCATCAAGGGGTGTGTGAACTGTCTTCACTGAGCCG 1908
 Qy 182 GAACAAGACATATGCTGCTCACTTAAGGGGTCTGTATCCAGATGTACACCAATGTGAGCC 241
 Db 1909 GAACAGAGACATCCGCTTCAACCAAGGGTCTGTCTATCCAGATGTATCAATGTAGACC 1968
 Qy 242 AAGACTGTGAGGTGCGCCGCTCCCAAGGTGCGCGCTCATTTAACCAATGCACTTGGC 301
 Db 1969 AAGACTGTGAGGTGCGCCGCTCCCAAGGTGAGCGCTCATTTGACACCTGCACTTGGC 2028
 Qy 302 GCTCTCTGGACCTTTAATCTGTGTCAAGAGCAAGCGGATGTCACTTGTGTGCGCCAGCGG 361
 Db 2029 GCTCTCTGGACCTTTAATCTGTGTCAAGAGCAAGCGGATGTCACTTGTGTGCGCGG 2088
 Qy 362 GTGATGGGAGGGGAGCGCTTGGCCCGGCGCTATCTTACTTGAAGGCTCTGGG 421
 Db 2089 GTGATGAGAGGGGAGCGCTGTGTGTGCGCCGCGCTATCTTACTTGAAGGCTCTGGG 2148
 Qy 422 GAGGCGCTGTGTGTGCGCCGCGAGACATGCGTAGGCAATTTCAAGAGCGCGGTATGCA 481
 Db 2149 GGGGTCGCTGTGTGTGCGCCGCGGAGCAAGCGGTGGGATTTAGGGCGCGGTGTGCA 2208
 Qy 482 CCCGTGAGAGTGGCTAAGGGGTGTGAGACTTATCCCGTAGAGCTTTAGACACATGCA 541
 Db 2209 CCCGTGAGAGTGGCTAAGGGGTGTGAGACTTATCCCGTAGAGACCTTAGAGACATGCA 2268
 Qy 542 GGTCCCGGCTGTCTCAAGCACTCTCCCAAGAGTGGCCCAAGACTTCAAGTGG 601
 Db 2269 GGTCCCGGCTGTCTCAAGCACTCTCTCTCAAGAGTGGCCCAAGACTTCTCAAGTGG 2328
 Qy 602 CCCACTGTGATGCTCCACCGGCAAGGCTAAGAGCAACCAAGTCCCGCGCATACGCA 661
 Db 2329 CTCACCTCATGCTCCACAGGCAAGGCAAGAAAGCAACCAAGTCCCGGTGATATGCA 2388
 Qy 662 CTCAGGGCTAAGAGTGTGTGTCAACCCCTCGGTGTCTGCAACATAGGCTTTGGTG 721
 Db 2389 CTCAGGGCTAATAGGTGTGTGTGTCAACCCCTCTGTGTCTCAACATAGGCTTTGGTG 2448
 Qy 722 CTATATGTCGAAGGCCATAGGATTTGATCTTAATCAAGCACTGGGGGTGAGAACATTA 781
 Db 2449 CTATATGTCGAAGGCTCATAGGATTCATCTTAATCAAGCACTGGGGGTGAGAACATTA 2508
 Qy 782 CTACTGTGAGCCGCACTCAAGTATTCACCGGCAAGTTCCTTGGCGACGCGGGTGT 841
 Db 2509 CCACGTGGAGCCGCACTCAAGTATTCACCGGCAAGTTCCTTGGCGACGCGGGTGT 2568
 Qy 842 CAGGGGTGTCTTATGACATTAATTTGTGACGAGTGCATCTCAACGATGCAATGCA 901
 Db 2569 CAGGGGTGTCTTATGACATTAATTTGTGACGAGTGCATCTCAACGATGCAATGCA 2628
 Qy 902 TCTTGGGCAATTGGCACTGTCTTGAACAGAGCAAGCGGGGGGAGAACATGACTGTGC 961
 Db 2629 TCTTGGGCAATTGGCACTGTCTTGAACAGAGCAAGCGGGGGGAGAACATGACTGTGC 2688
 Qy 962 TCGCACGCGTACCCCTCGGGCTCGGTCACTGTGCGCATTCCAACATCGAGAGTTG 1021
 Db 2689 TCGCACGCGGCAACCCCTCGGGCTCGGTCACTGTGCGCATTCCAACATCGAGAGTTG 2748
 Qy 1022 CTCTGTCCACTACCGGAGAGATCCCTTTTATGGCAAGGCTATTCCTCTTGAAGCAATTA 1081
 Db 2749 CTCTGTCCACTACCGGAGAGATCCCTTTTATGGCAAGGCTATTCCTCTTGAAGCAATTA 2808
 Qy 1082 AGGGGGGAGACATCTCATCTTCTGCACTCAAGAGAGGCGAGCGAGCTCGCGGCA 1141
 Db 2809 AGGGGGGAGACATCTCATCTTCTGCACTCAAGAGAGGCGAGCGAGCTCGCGGCA 2868
 Qy 1142 AACTGTGCGCTTGGGCGTCAATGCGGTGCTTAACCGCGGCTTGAATGTGTCTGCTCA 1201

Db 2869 AGCTGTGCAATTGGGACATCAATGCCGTGGCCCTACTACCGCGGTCTTGAAGTGTCCGTCA 2928
 Qy 1202 TCCGAGACAGTGTGACGTTGTGTGTGTGCAATGAGCGCCCTCAATGACCGGCTTTACCG 1261
 Db 2929 TCCGAGACAGCGGACATGTGTGTGTGTGTGCAATGAGCGGCTCTCAATGACCGGCTTTACCG 2988
 Qy 1262 GCGACTTGCAATTCGATGTAGACTGCAACAGTGTGTGCAACCGAGACAGTGTGACTTACGCC 1321
 Db 2989 GCGACTTGCACTCGATGTAGACTGCAATGAGTGTGTGCAACCGAGACAGTGTGACTTACGCC 3048
 Qy 1322 TTGACCTTACCTTCAACATTTGACATCAAGCTTCCCGAGATGTGTCTCCGTACTTC 1381
 Db 3049 TTGACCTTACCTTCAACATTTGACATCAAGCTTCCCGAGATGTGTCTCCGTACTTC 3108
 Qy 1382 AACGTGCGGGTATGAGCTGGCAAGGGAAGCCAGGATCTACATTTTGTGGCACCGGGG 1441
 Db 3109 AACGTGCGGGTATGAGCTGGCAAGGGAAGCCAGGATCTACATTTTGTGGCACCGGGG 3168
 Qy 1442 AGCGTCTTCTTGGCACTGTTTGACTGTGTGTCTGTGCGAGTGTATGACGCGGGTGTG 1501
 Db 3169 AGCGCGCTTCCGCAATGTTCAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 3228
 Qy 1502 CTTGGTATGAGCTTACGCGCCCGGAGACCAAGTTAGGCTACAGCATTCATGAACACC 1561
 Db 3229 CTTGGTATGAGCTTACGCGCCCGGAGACTACAGTTAGGCTACAGCATTCATGAACACC 3288
 Qy 1562 CGGACCTTCCGCTGTGCGCAAGCACTTTGAATTTTGGAGGGCGCTTTTACGGGCTCA 1621
 Db 3289 CGGACCTTCCGCTGTGCGCAAGCACTTTGAATTTTGGAGGGCGCTTTTACGGGCTCA 3348
 Qy 1622 CCCACATGACGCGCACTTCTATCCAGACAAAGAGTGGGGAACCTTCCCTATC 1681
 Db 3349 CTCATATGATATGCCACTTTCTATCCAGACAAAGAGTGGGGAACCTTCCCTATC 3408
 Qy 1682 TGGTAGCGTACCAAGCCACGCTGTGCGCTAGAGCTCAAGCCCTTCCCGTGTGGAGCC 1741
 Db 3409 TGGTAGCGTACCAAGCCACGCTGTGCGCTAGAGGCTCAAGCCCTTCCCGTGTGGAGCC 3468
 Qy 1742 AGATGTGAGAGTGTGATTCGCTCAAGCCCACTCCATAGGGGCAACCTGTGTAT 1801
 Db 3469 AGATGTGAGAGTGTGATTCGCTCAAGCCCACTCCATAGGGGCAACCTGTGTAT 3528
 Qy 1802 ATGACTGCGGCTGTCCAGATGGAATGAGTCAACCTGACGCAACCATGATATATCA 1861
 Db 3529 ATGACTGCGGCTGTCCAGATGGAATGAGTCAACCTGACGCAACCATGATATATCA 3588
 Qy 1862 TGAATGTATGTGCGCTGAAGTGTGTCAAGATGCTGAGTGTGCTGTGGCGGCG 1921
 Db 3589 TGAATGTATGTGCGCGCGCTGAGAGTGTGTCAAGACCTGTGGGTGCTGTGGCGGCG 3648
 Qy 1922 TTTGTGCTGCTTTGGCGCGGTATTTGCTTATCAAGCGCTGCTGTATAGTAGTAGGA 1981
 Db 3649 TTTGTGCTGCTTTGGCGCGGTATTTGCTTATCAAGCGCTGCTGTATAGTAGTAGGA 3708
 Qy 1982 TTTGTGCTGCGGAAGCGGCAATCATACCCGACAGGGAATGCTTACCGGAGTTG 2041
 Db 3709 TTTGTGCTGCGGGAAGCGGCAATCATCTGACAGGGAATGCTTACCGAGAGTTG 3768
 Qy 2042 ATGAATGGAAGAGTGTCT 2059
 Db 3769 ATGAATGGAAGAGTGTCT 3786

RESULT 7
 AAN90336
 ID AAN90336 standard; DNA; 7310 BP.
 XX
 AC AAN90336;
 XX
 XX
 DT 25-MAR-2003 (revised)
 DT 19-JUL-2001 (revised)
 DT 01-NOV-1989 (first entry)
 XX

DE Composite hepatitis C virus (HCV) cDNA.
XX Hepatitis C virus; cDNA; clone 15e; clone k9-1; probe; vaccine; ds.
XX Pan ctyoglobydes.
OS GB212511-A.
XX 26-JUL-1989.
XX 18-NOV-1988; 88GB-00027024.
XX PF 18-NOV-1987; 87US-00122714.
XX PR 30-DEC-1987; 87US-00139866.
XX PR 26-FEB-1988; 88US-00161072.
XX PR 26-OCT-1988; 88US-00263584.
XX PA (CHIR) CHIRON CORP.
XX PI Houghton M, Choo QL, Kuo G;
XX WPI; 1989-215054/30.
XX DR P-PSDB; AAP90288.
XX PT Hepatitis C virus gene - used for prodn. of polynucleotide probes
XX PT polypeptide(s) and antibodies for diagnosis, prevention and treatment of
XX PT infection.
XX PS Disclosure; Fig 47; 30pp; English.
XX The sequence shows a composite hepatitis C virus (HCV) cDNA, derived by
XX aligning clones k9-1 through 15e in 5'-3' direction. The cDNA encodes
XX antigens which react with antibodies in patients with non-A non-B
XX hepatitis (NANBH). The cDNA can be used to design probes, or to
XX synthesize polypeptides, which are used to diagnose HCV-induced NANBH, to
XX raise antibodies for immunosassay or treatment, or to produce vaccines.
XX See also AAP90288, and AAN90303-35. (N.B. This record was resubmitted to
XX correct errors in the sequence.) (Updated on 25-MAR-2003 to correct PR
XX field.)
SQ Sequence 7310 BP; 1495 A; 2218 C; 2058 G; 1539 T; 0 U; 0 Other;
Query Match 86.7%; Score 1786; DB 1; Length 7310;
Query Local Similarity 91.7%; Pred. No. 0;
Matches 1888; Conservative 0; Mismatches 170; Indels 0; Gaps 0;
QY 2 TGGCGCTATACGCGCTATGCCCAGACAGACAAAGGGGCTTTGGAGTGCATATACCA 61
DB 1729 TGGCGCCATACAGGCGTACGCCAGACAGACAAAGGGGCTTCTAGGGTGCATATACCA 1788
QY 62 GCTTGACCGGCGCGGACAAACCAAGTGAAGGTGAGTTCAGATCGTGTCAACTGCTG 121
DB 1789 GCTTAACTGGCGGGACAAACCAAGTGAAGGTGAGTTCAGATCGTGTCAACTGCTG 1848
QY 122 CCCAGACTTTTGGCAACTGCAATTAAGGGGTGTGGAATGCTCTACATGAGCCG 181
DB 1849 CCCAAACCTTCTGCGACATGTCATTAAGGGGTGTGGAATGCTCTACATGAGCCG 1908
QY 182 GAACAGAGCAATGCGTCACTTAAGGGTCTGTATCCAGATGTAACCAATGTGACC 241
DB 1909 GAACAGAGCAATGCGTCACTTAAGGGTCTGTATCCAGATGTAACCAATGTGACC 1968
QY 242 AAGACTCTGTAGGTGCGGCTCCCGCAAGTGGCCGCTCAATTAACCAATGTGACC 301
DB 1969 AAGACTCTGTAGGTGCGGCTCCCGCAAGTGGCCGCTCAATTAACCAATGTGACC 2028
QY 302 GCTCCCTGAGACCTTTACTGTGTACAGAGGACGCGCATGCTCTGCGCCGAC 361
DB 2029 GCTCCCTGAGACCTTTACTGTGTGTACAGAGGACGCGCATGCTCTGCGCCGAC 2088
QY 362 GTGATGGCAGGGGACAGCTGTCTTTCGCGCGGCTTATCTTAAAGGCTCTCTCG 421
DB 2089 GTGATGGCAGGGGACAGCTGTCTTTCGCGCGGCTTATCTTAAAGGCTCTCTCG 2148

QY 422 GAGGCGCTGTGCTGNGCCCGCAGAGACATGCGATATTAGAGCCGCGGTATGCA 481
DB 2149 GAGGCTCCCTGTGTGCCCCCGGAGCAGCGCTGTGAGGATTTTGAAGCCGCGGTGTGCA 2208
QY 482 CCCGTGAGTGTGCTAAGGCGGTGACCTTCATCCCGTGAAGAGCTTAGAGCAACATGA 541
DB 2209 CCCGTGAGTGTGCTAAGGCGGTGAGCTTATCCCTGTGAGAGAACTTAGAGCAACATGA 2268
QY 542 GGTCCCGGTGTGCTGACAGCAATCTCTCCCAACAGAGTGGCCCAAGCTAACAGTGG 601
DB 2269 GGTCCCGGTGTGCTGACAGCAATCTCTCCCAACAGAGTGGCCCAAGCTAACAGTGG 2328
QY 602 CCCACCTGATGCTCCACCGGACGCGGTAAAGAGCAAGGTCCCGGCGGATCGCAG 661
DB 2329 CTACCTCAGTCTCCACAGGACGCGGAAAGCAAGAGTCCCGGCTGATATGCA 2388
QY 662 CTACAGGCTAAGAGTGTGTGCTCAACCCCTCCGTGCTGCAACATGGGCTTTGGTG 721
DB 2389 CTACAGGCTAAGAGTGTGTGCTCAACCCCTCCGTGCTGCAACATGGGCTTTGGTG 2448
QY 722 CTACATGTCCAGAGCCCATGGATGATCTCTACATCAGAGCTGGGTGAGACATTA 781
DB 2449 CTACATGTCCAGAGCCCATGGATGATCTCTACATCAGAGCTGGGTGAGACATTA 2508
QY 782 CTACTGGAGCCCGATCAGTATTCACCTACGCGCAAGTCCCTGCGAGCGGGGTGT 841
DB 2509 CCACTGGAGCCCGATCAGTATTCACCTACGCGCAAGTCCCTGCGAGCGGGGTGT 2568
QY 842 CAGGGGTGCTTATGACATTAATTGTGACAGATGTCACCTCAAGATGACATCA 901
DB 2569 CAGGGGTGCTTATGACATTAATTGTGACAGATGTCACCTCAAGATGACATCA 2628
QY 902 TCTTGGGATTTGGCACTGTCTTGTACCAAGAGAACCGCGGGGCGAGACTGATCTGC 961
DB 2629 TCTTGGGATTTGGCACTGTCTTGTGTGCAAGAGAACCGCGGGGCGAGACTGATCTGC 2688
QY 962 TCGGACCGCTACCCCTCGGGCTCGATGCTGTCAGTGGCCCATCTTAACATCGAGAGTGG 1021
DB 2689 TCGGACCGCTACCCCTCGGGCTCGATGCTGTCAGTGGCCCATCTTAACATCGAGAGTGG 2748
QY 1022 CTCTGTCCATCAACCGAGAGATCCCTTTTATGCGAGGCTATTCCTTTGAAGCAATTA 1081
DB 2749 CTCTGTCCATCAACCGAGAGATCCCTTTTATGCGAGGCTATTCCTTTGAAGCAATTA 2808
QY 1082 AGGGGGGAGACATCTTCTTCTGCACTCAAAAGAAAGTGGCAGAGCTCCCGGCA 1141
DB 2809 AGGGGGGAGACATCTTCTTCTGCACTCAAAAGAAAGTGGCAGAGCTCCCGGCA 2868
QY 1142 AACTGTGCGGTGGGCGTCAATGCGGTGCTTACACGCGGCTTGATGTGCTCGTCA 1201
DB 2869 AACTGTGCGGTGGGCGTCAATGCGGTGCTTACACGCGGCTTGATGTGCTCGTCA 2928
QY 1202 TCCCGACAGAGTGTGACCTGTGTGTGCAATGACGCGCTCATGACGCGCTTTACG 1261
DB 2929 TCCCGACAGAGTGTGACCTGTGTGTGTGCAATGACGCGCTCATGACGCGCTTTACG 2988
QY 1262 GCGACTTGTGATTCGTGATGACCTGCAACAGTGTGTCAACCGACAGCTTCAAGCC 1321
DB 2989 GCGACTTGTGATTCGTGATGACCTGCAACAGTGTGTCAACCGACAGCTTCAAGCC 3048
QY 1322 TTGACCTTACCTTCAACATTAAGACATCAAGCTTCCCGAGATGCTGCTCCGTAATC 1381
DB 3049 TTGACCTTACCTTCAACATTAAGACATCAAGCTTCCCGAGATGCTGCTCCGTAATC 3108
QY 1382 AACGTGCGGGTGAAGCTGGCAGAGGAAAGCCAGGATCTACAGATTTGTGGACCGGGG 1441
DB 3109 AACGTGCGGGTGAAGCTGGCAGAGGAAAGCCAGGATCTACAGATTTGTGGACCGGGG 3168
QY 1442 AGCGTCTTCTGGGATGTTTGAATGCTGTCTCTGCGAGTGTGATACGCGGGTGG 1501
DB 3169 AGCGTCTTCTGGGATGTTTGAATGCTGTCTCTCTGAGAGTGTGATGACGAGGCTGTG 3228


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QY 1502 CTTGGTATGAGCTTACGCCCCGCGAGACCACTTATGAGCTACAGCATATGAAACACC 1561
DB 3229 CTTGGTATGAGCTACGCCCCGCGAGACCTACAGTATGAGCTACAGTAAACACC 3288
QY 1552 CGGGACTTCCGCTGCGCAAGACCATCTTGAATTTTGGAGGCGCTTTTACGGGCTCA 1621
DB 3289 CGGGGCTTCCGCTGCGCAAGACCATCTTGAATTTTGGAGGCGCTTTTACAGGCTCA 3348
QY 1652 CCCACATGAGGCGCACTTCCATCCGACCAAGAGAGTGGGAAAACCTTCCCTATC 1681
DB 3349 CTCATATGAGTCCCACTTTCTATCCGACCAAGAGAGTGGGAAAACCTTCTTACC 3408
QY 1682 TGGTAGCGTACCAAGCAGCAGTGTGCGTAGAGCTCAAGCCCTCCCGCTGTGAGACC 1741
DB 3469 TGGTAGCGTACCAAGCAGCAGTGTGCGTAGAGCTCAAGCCCTCCCGCTGTGAGACC 3468
QY 1742 AGATGTGAGAGTCTTGTATCGCTCTCAAGCCCACTCCATGGGCAACACCTGTCTAT 1801
DB 3469 AGATGTGAGAGTCTTGTATCGCTCTCAAGCCCACTCCATGGGCAACACCTGTCTAT 3528
QY 1802 ATAGACTGGGCGCTGTCCAGAAATGAGTCAAGCTGACGACCCAGTCAACAGTATATCA 1861
DB 3529 ACAGACTGGGCGCTGTGTGAGAAATGAGTCAAGCTGACGACCCAGTCAACAGTATATCA 3588
QY 1862 TGACATGATATGTGCGCTGACCTGAGAGTGTGTCACAGTACTGGGTGCTGTTGGCGCG 1921
DB 3589 TGACATGATATGTGCGCTGACCTGAGAGTGTGTCACAGTACTGGGTGCTGTTGGCGCG 3648
QY 1922 TTTGCTGCTTGTGGCGCGCTATTTGCTATTCACAGGCTGCGTGTCAATGATGATGAGA 1981
DB 3649 TCTGCTGCTTGTGGCGCGCTATTTGCTATTCACAGGCTGCGTGTCAATGATGATGAGA 3708
QY 1982 TTTGCTGCTTGTGGCGCGCTATTTGCTATTCACAGGCTGCGTGTCAATGATGATGAGA 2041
DB 3709 TCGTCTTGTGCGGGAAGCGGGAATCTATCTGACAGAGGAAGTCTCTTACCGAGAGTTG 3768
QY 2042 ATGAATGAGAGAGTGTCT 2059
DB 3769 ATGAATGAGAGAGTGTCT 3786

RESULT 8
AAQ98221
ID AAQ98221 standard; cDNA to mRNA; 7310 BP.
XX
AC AAQ98221;
XX
DT 25-MAR-2003 (revised)
DT 15-AUG-1996 (first entry)
XX
DE Hepatitis C virus clone genome.
XX
KM Hepatitis C virus; HCV; antigen; detection; diagnosis; vaccine;
KM antibodies; immunoprophylaxis; sera; serum; ds.
OS Hepatitis C virus.
XX
PN US5443965-A.
XX
PD 22-AUG-1995.
XX
PF 05-APR-1991; 91US-00681703.
XX
PR 06-APR-1990; 90US-00505611.
XX
PR 09-OCT-1990; 90US-00594854.
XX
PA (GENE-) GENELABS INC.
XX
PI Moeckli R, Reyes GR, Kim JP;
DR WPI; 1995-302120/39.
XX
PT New nucleic acids encoding hepatitis C virus antigens - used to develop
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PT prods. for detection of HCV-infected sera and prodn. of vaccines and anti
PT -HCV antibodies.
XX
PS Example 4; Fig 11; 71pp; English.
XX
CC Hepatitis C virus (HCV) antigens can be used for detecting HCV infected
CC sera and individuals infected with HCV. They can also be used in an anti-
CC HCV vaccine or for the production of anti-HCV antibodies which can be
CC used for passive immunoprophylaxis. The antigens consistently identify
CC more HCV positive serum samples with a high degree of specificity. See
CC AAQ98202-14 and AAR81939-51. (Updated on 25-MAR-2003 to correct PF
CC field.) (Updated on 25-MAR-2003 to correct PR field.)
SQ
Sequence 7310 BP; 1494 A; 2217 C; 2060 G; 1539 T; 0 U; 0 Other;

Query Match 86.7%; Score 1786; DB 2; Length 7310;
Best Local Similarity 91.7%; Pred. No. 0;
Matches 1888; Conservative 0; Mismatches 170; Indels 0; Gaps 0;

2 TGGGCGCTATCAAGGCTATGCGCCAGACAGCAAGGGGCTTTGGGATGATATACCA 61
DB 1729 TGGGCGCTATCAAGGCTATGCGCCAGACAGCAAGGGGCTCTTAGGGTGCATATACCA 1788
QY 62 GCTTACCGGCGCGGACAAAACAGGTGAGAGGTGAGGTTGATGATGCTGCACTGCTG 121
DB 1789 GCTTACCGGCGCGGACAAAACAGGTGAGAGGTGAGGTTGATGATGCTGCACTGCTG 1848
QY 122 CCCAAGCTTTCTTGGCAACCTGCAATTAAGGGGTGTGTGATCTGTACCATGAGCCG 181
DB 1849 CCCAAGCTTTCTTGGCAACCTGCAATTAAGGGGTGTGTGATCTGTACCATGAGCCG 1908
QY 1849 GAAAGAGGACATAGCGTACCTAAGGGTCTGTATCCAGATGATACCAATGTGAGACC 241
DB 1909 GAAAGAGGACATAGCGTACCTAAGGGTCTGTATCCAGATGATACCAATGTGAGACC 1968
QY 242 AAGACCTGTAGAGTGGCGCGCTCCCAAGGTGCGCGCTCATTAACACCATGACCTTGG 301
DB 1969 AAGACCTGTAGAGTGGCGCGCTCCCAAGGTGCGCGCTCATTAACACCATGACCTTGG 2028
QY 302 GCTCTCTGGAACCTTTTACTGCTGTACAGAGGACCGGATGTCACTCTGTGGCGCAAGG 361
DB 2029 GCTCTCTGGAACCTTTTACTGCTGTACAGAGGACCGGATGTCACTCTGTGGCGCAAGG 2088
QY 362 GTGATGAGAGGGGAGCGCTGTGGCGCGCGCTATCTTACTTGAAGGCTCCTCGG 421
DB 2089 GTGATGAGAGGGGAGCGCTGTGGCGCGCGCTATCTTACTTGAAGGCTCCTCGG 2148
QY 422 GAGGCGCTCTGTGTGCGCGCGAGACATGCGGTAGAGCATATTCAGAGCGCGGTATGCA 481
DB 2149 GAGGCGCTCTGTGTGCGCGCGAGACATGCGGTAGAGCATATTCAGAGCGCGGTATGCA 2208
QY 482 CCGGTGAGGTGCTAAGGCGGTGACCTTCATCCCGGTAGAGAGCTTTAGAGCAACCATCA 541
DB 2209 CCGGTGAGGTGCTAAGGCGGTGACCTTCATCCCGGTAGAGAGCTTTAGAGCAACCATCA 2268
QY 542 GGTCCCGGTGTTTCAAGATTAACCTCTTCCACAGATGTGCGCCAGAGCTTCCAGGTG 601
DB 2269 GGTCCCGGTGTTTCAAGATTAACCTCTTCCACAGATGTGCGCCAGAGCTTCCAGGTG 2328
QY 602 CCCACTGATGCTCCACCGGCAAGGTAAAGAGCAAGAGTCCCGGCGCATATGCGAG 661
DB 2329 CTCACCTCATGCTCCACAGGCAAGGCAAGAGCAAGAGTCCCGGCGCATATGCGAG 2388
QY 662 CTCAGGGCTCAAGGTGCTGTGCTCAACCCCTCGGTGTGCAACAAATGGGCTTTGGTG 721
DB 2389 CTCAGGGCTCAAGGTGCTGTGCTCAACCCCTCGGTGTGCAACAAATGGGCTTTGGTG 2448
QY 722 CTTAATGTCAGAGGCGCATGAGATTGATTCCTAATCAGAGCTGAGGGGTAGAGCAATTA 781
DB 2449 CTTAATGTCAGAGGCGCATGAGATTGATTCCTAATCAGAGCTGAGGGGTAGAGCAATTA 2508
QY 782 CTAAGTGGAGCGGATCAAGTATTCACCTTACGAGCAAGTCTTGGCCGAGCGGAGTGT 841
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Db 2509 CCACTGGACGCCCATACGTACTCCACCTACGGCAAGTTCCTTGCCGACGGCGGGTGT 2568
Qy 842 CAGGGGGGTCTTATGACATTAATTTTGGAGAGTGGCCACTCCAGGTGCAATCA 901
Db 2569 CGGGGGGCGCTTATGACATTAATTTTGGAGAGTGGCCACTCCAGGTGCAATCA 2628
Qy 902 TCTTGGGCAATGGACCTGTCTTGGACCAAGAGACGGGGGGGAGACTGACGTGTC 961
Db 2629 TCTTGGGCAATGGACCTGTCTTGGACCAAGAGACTGGGGGGGAGACTGTTGTTC 2688
Qy 962 TGGCCACCGCTACCCCTCCGGGCTCCGTACTGTGCCCCCTCAATCAGAGAGTTG 1021
Db 2689 TGGCCACCGCCACCCCTCCGGGCTCCGTACTGTGCCCCCTCAATCAGAGAGTTG 2748
Qy 1022 CTCTGTCCACTACCGGAGAGATCCCTTTTATGGCAAGCTATTCCCTTGAAGCAATTA 1081
Db 2749 CTCTGTCCACTACCGGAGAGATCCCTTTTATGGCAAGCTATTCCCTTGAAGCAATCA 2808
Qy 1082 AGGGGGGGAGACATCTCATCTTCTGCACTCAAAAGAAAGTGGCAGAGCTCGCGCA 1141
Db 2809 AGGGGGGGAGACATCTCATCTTCTGCACTCAAAAGAAAGTGGCAGAGCTCGCGCA 2868
Qy 1142 AACTGTCGCTTGGGCGTCAATGCGGTGCTTACTACCGCGCTTGATGTGTCGTCA 1201
Db 2869 AACTGTCGCTTGGGCGTCAATGCGGTGCTTACTACCGCGCTTGATGTGTCGTCA 2928
Qy 1202 TCCCGACCAAGTGTGACGTTGTGCTGTGGCACTGACGCGCTCATGACGCGCTTACCG 1261
Db 2929 TCCCGACCAAGTGTGACGTTGTGCTGTGGCACTGACGCGCTCATGACGCGCTTACCG 2988
Qy 1262 GCGACTTGCATTCGGGTAGACTGCAACAGCTGTGTCAACCGACAGTGCATTCAGCC 1321
Db 2989 GCGACTTGCATTCGGGTAGACTGCAACAGCTGTGTCAACCGACAGTGCATTCAGCC 3048
Qy 1322 TTGACCCCTACCTTCAACCATTTGAACAATCAGCTTCCCGAGAGTGTCTCCGTACTC 1381
Db 3049 TTGACCCCTACCTTCAACCATTTGAACAATCAGCTTCCCGAGAGTGTCTCCGTACTC 3108
Qy 1382 AACGTCGGGGTAGACTGGCAGAGGGAAGCCAGGCTCTACAGATTTTGGGACCGGGGG 1441
Db 3109 AACGTCGGGGTAGACTGGCAGAGGGAAGCCAGGCTCTACAGATTTTGGGACCGGGGG 3168
Qy 1442 AGCGTCTCTTGGAGATTTTGAAGTCTGTCTGTCTGAGAGTCTATGACGGGGTGTG 1501
Db 3169 AGCGTCTCTTGGAGATTTTGAAGTCTGTCTGTCTGAGAGTCTATGACGGGGTGTG 3228
Qy 1502 CTTGGTATGAGCTTACGCGCGCGGAGACCAAGTTAGGCTACGAGCATACATGAACCC 1561
Db 3229 CTTGGTATGAGCTTACGCGCGCGGAGACCAAGTTAGGCTACGAGCATACATGAACCC 3288
Qy 1562 CGGGACTTCCCGTGGCCAAAGACATTTTGGAGGGCGCTTTACGGGTCTCA 1621
Db 3289 CGGGGCTTCCCGTGGCCAAAGACATTTTGGAGGGCGCTTTACGGGTCTCA 3348
Qy 1622 CCCACATAGACGCCCACTTCTATCCAGACAAGAGAGTGGGGAAAACCTTCCCTATC 1681
Db 3349 CTCATATAGATGCCCACTTCTATCCAGACAAGAGAGTGGGGAAAACCTTCCCTATC 3408
Qy 1682 TGGTACCGTACCAAGCCAGTGTGCGCTAGAGCTCAAGCCCTCCCGCTGTGGAGCC 1741
Db 3409 TGGTACCGTACCAAGCCAGTGTGCGCTAGAGCTCAAGCCCTCCCGCTGTGGAGCC 3468
Qy 1742 AATATGTGGAAGTGTGATCCGTCTCAAGCCCACTCCATGGGCCAACAACCTTGTCTAT 1801
Db 3469 AATATGTGGAAGTGTGATCCGTCTCAAGCCCACTCCATGGGCCAACAACCTTGTCTAT 3528
Qy 1802 ATAGACTGGGCGCTGTCCAGAAATGAAGTCAACCTGACGACCAAGTCAAGATATATCA 1861
Db 3529 AAGAGCTGGGCGCTGTCCAGAAATGAAGTCAACCTGACGACCAAGTCAAGATATATCA 3588
Qy 1862 TGAATATATATGTGTGAGCTGACCTTGAAGTGTCTCAAGATATATATATATATATATCA 1921
Db 3589 TGAATATATATGTGTGAGCTGACCTTGAAGTGTCTCAAGATATATATATATATATATCA 3648

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Qy 1922 TTCTGGCGCTTTTGGCGCGGATTTGCTTATCCACAGGCTGGGTGTCTATGATGAGTAA 1981
Db 3649 TCTGGCGCTTTTGGCGCGGATTTGCTTATCCACAGGCTGGGTGTCTATGATGAGTAA 3708
Qy 1982 TTTGCTTGTCCGGAAGCGGCAATCATATCCGACAGGAAAGTCTCTTACCGGGAGTTG 2041
Db 3709 TGTGCTTGTCCGGAAGCGGCAATCATATCCGACAGGAAAGTCTCTTACCGAGATTG 3768
Qy 2042 ATGAATGGAAGAGTGTCT 2059
Db 3769 ATGAGATGGAAGAGTGTCT 3786

RESULT 9
AAA75296
ID AAA75296 standard; cDNA, 8316 BP.
XX
XX AAA75296;
AC 15-JAN-2001 (first entry)
XX
XX cDNA sequence compiled Hepatitis C virus cDNA clones.
DE Hepatitis C virus; HCV; antisense polynucleotide; polypeptide;
KM viral infectivity; viral replication; de.
XX Hepatitis C virus.
OS
FH Key Location/Qualifiers
FT 1. 8316
FT CDS /tag= a
FT FT /note= "partial sequence; no termination codon given"
XX
XX EPI034785-A2.
PN 13-SEP-2000.
XX
XX 16-MAR-1990; 2000EP-00109602.
PR 17-MAR-1989; 89US-00325338.
PR 20-APR-1989; 89US-00341334.
PR 18-MAY-1989; 89US-0035002.
PR 16-MAR-1990; 90EP-00302866.
XX
XX (CHIR ) CHIRON CORP.
XX
XX Houghton M, Choo Q, Kuo G;
PI WPI: 2000-566891/53.
XX P-PSDB; AAB18540.
DR
XX
XX Novel composition comprising a hepatitis C virus antisense polynucleotide
PT which is complementary to or corresponds to a sense strand of the virus
PT genome, and selectively hybridizes to it.
XX
XX Example: Fig 16; 75pp; English.
XX
XX The specification describes a pharmaceutical composition which comprises
XX a hepatitis C virus (HCV) antisense polynucleotide. The HCV is
XX characterized by a positive stranded RNA genome which has 40% homology at
XX the polypeptide level to a HCV polypeptide. The antisense polynucleotide
XX binds to cellular polynucleotides which enhance and/or are required for
XX viral infectivity, replicative ability or chronicity. The antisense
XX polynucleotides may also be designed to bind with high specificity, to be
XX of increased stability, to be stable and to have low toxicity. The
XX composition also comprises an agent which causes viral RNA to be
XX inactive. The composition is used for preventing HCV replication in a
XX system. The present sequence represents a novel HCV cDNA sequence, which
XX is used in the course of the invention
XX
XX Sequence 8316 BP; 1671 A; 2529 C; 2345 G; 1771 T; 0 U; 0 Other;
XX

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|----------------------------|------|--|
| Query Match | | 86.7%; Score 1786; DB 3; Length 8316; |
| Best Local Similarity | | 91.7%; Pred. No. 0; |
| Matches 1888; Conservative | | 0; Mismatches 170; Indels 0; Gaps 0; |
| QY | 2 | TGGCCCTATCAAGGCTTATGCGCCAGAGACAAAGGGCTTTTGGAGTCATATACCA 61 |
| DB | 2735 | TGGCCCTATCAAGGCTTATGCGCCAGAGACAAAGGGCTTTTGGAGTCATATACCA 2794 |
| QY | 62 | GCTTACGGGGGAGCAAAAACGAGTGGAGGTGAGGTTGAGTTCGATCGTCAACTGGCG 121 |
| DB | 2795 | GCTTACGGGGGAGCAAAAACGAGTGGAGGTGAGGTTGAGTTCGATCGTCAACTGGCG 2854 |
| QY | 122 | CCAGACTTTCTTGGCAACTGCAATTAAGGGTGTGTGACGTGTCACTGACAGAGCCG 181 |
| DB | 2855 | CCCAAACTTCTTGGCAAGTGCATCAAGGGTGTGTGACGTGTCACTGACAGAGCCG 2914 |
| QY | 182 | GAACAAGACATTTGGCTACCTTAAGGTCTGTGTTATCCAGATGTACCAATGTGAGC 241 |
| DB | 2915 | GAACAAGACATTTGGCTACCTTAAGGTCTGTGTTATCCAGATGTATCAATGTGAGC 2974 |
| QY | 242 | AAGACTGTAGGCTGAGCGCGCTCCCGCAAGTGGCCGCTCATTAACACATGCACTGGC 301 |
| DB | 2975 | AAGACTGTGTGGCTGAGCGCGCTCCCGCAAGTGGCCGCTCATTAACACCTGCACTGGC 3034 |
| QY | 302 | GCTCTCGGACCTTTAAGCTGTACAGAGGACGCGAGTGTCAATCTGTGCGCGACGG 361 |
| DB | 3035 | GCTCTCGGACCTTTAAGCTGTACAGAGGACGCGAGTGTCAATCTGTGCGCGCGGG 3094 |
| QY | 362 | GTGATGGAGGGGACGCTGCTTTGCGCCCGGCTATCTTTACTTGAAGGCTCTCTCG 421 |
| DB | 3095 | GTGATGAGCGGGGACGCTGCTGTGCGCCCGGCTATCTTTACTTGAAGGCTCTCTCG 3154 |
| QY | 422 | GAGGCTCTGTGCTGTGCGCCCGAGACATGCGGTGAGCATTTACAGAGCGGGATGTGA 481 |
| DB | 3155 | GAGGCTCTGTGCTGTGCGCCCGAGAGCGCGGTGAGCATTTATGAGCGGGGTGTGA 3214 |
| QY | 482 | CCCGTGGAGTGGCTAAGCGGTGAGCTTCAATCCCGTAGAGACTTAGAGCAACATGA 541 |
| DB | 3215 | CCCGTGGAGTGGCTAAGCGGTGAGCTTATCCCTGTGAGAACCTTAGAGCAACATGA 3274 |
| QY | 542 | GGTGCCCGGTGTCTCAGACAACTCTCCCAACAGAGTGGCCCAAGCTACCAAGTG 601 |
| DB | 3275 | GGTGCCCGGTGTCTCAGAGTAACCTCTCCCAAGTAGTGCCCAAGACTTCCAGGTG 3334 |
| QY | 602 | CCCACCTGATGCTCCCAACGGGAGGGTAAGAGCACCAAGTCCCGGCGCATAGCG 661 |
| DB | 3335 | CTCAGCTCATGCTCCCAAGGAGGAGGCAAAAGCACCAAGTCCCGGCTGATAGCG 3394 |
| QY | 662 | CTCAGGGCTACAAAGGTGTGTGCTCAACCCCTCGTGTGCTGCAACAATGGGCTTTGGT 721 |
| DB | 3395 | CTCAGGGCTATTAAGGTGTGTGCTCAACCCCTCTGTGTGCTGCAACTGGGCTTTGGT 3454 |
| QY | 722 | CTTACATGTCAAGGCGCCATGGGATTTGATCTTAACATCAGAGCTGCGGTGAGACAATTA 781 |
| DB | 3455 | CTTACATGTCAAGGCTCATGGGATGATCTTAACATCAGAGCGGGGTGAGACAATTA 3514 |
| QY | 782 | CTACTGGGAGCGCCGATCAGATTTCACTTACAGGCAAGTTCTTGGCGAGCGGGTGT 841 |
| DB | 3515 | CCACTGGGAGCGCCATCAGTACTCACTACAGGCAAGTTCTTGGCGAGCGGGTGTCT 3574 |
| QY | 842 | CAGGGGGTGTATGACATATTAATTGTGAGAGTGCACCTCAAGGATGACATCCA 901 |
| DB | 3575 | CAGGGGGGCGTTATGACATATTAATTGTGAGAGTGCACCTCAAGGATGACATCCA 3634 |
| QY | 902 | TCTTGGGCAATTGGCACTGTCTTGAACAGACAGACCGCGGGGGGAGACTGATGTGC 961 |
| DB | 3635 | TCTTGGGCACTGGCACTGTCTTGAACAGACAGACTGCGGGGGGAGACTGATGTGC 3694 |
| QY | 962 | TGGCCACCGCTACCTCTCGGGCTCGTCACTGTGCGCCCATCTCTAACATGAGAGTTG 1021 |
| DB | 3695 | TGGCCACCGCACCTCTCGGGCTCGTCACTGTGCGCCCATCTCTAACATGAGAGTTG 3754 |
| QY | 1022 | CTCTGTCACTACCGGAGAGATCCCTTTTATGGCAAGGCTATTCCTCTTGAAGCAATTA 1081 |

| | | |
|----|------|--|
| DB | 3755 | CTCTGTCACTACCGGAGAGATCCCTTTTATGGCAAGGCTATTCCTCTCTGAAGTATCA 3814 |
| QY | 1082 | AGGGGGGAGACATCTCATCTTCTGCACTCAAAAAGAGTGCACAGGCTCGCGGAA 1141 |
| DB | 3815 | AGGGGGGAGACATCTCATCTTCTGCACTCAAAAAGAGTGCACAGGCTCGCGGAA 3874 |
| QY | 1142 | AACGTGTGCGGTGGGCGTCAATGCGCGTGTACTTACCGCGGCTTGTGTGCTGCA 1201 |
| DB | 3875 | AGCTGTGCGATTTGGGCTCAATGCGCGTGTACTTACCGCGGCTTGTGTGCTGCA 3934 |
| QY | 1202 | TCCCGACAGTGTGACGTTGTGTGTGCACTGACGCGCTCATGACGCGCTTTACCG 1261 |
| DB | 3935 | TCCCGACAGCGGCGATGTTGTGTGTGCACTGACGCGATCTCATGACGCGCTATACCG 3994 |
| QY | 1262 | GCGACTTGATTTGCGGTATAGCTGCAACAGCTGTGTCAACCCAGACGTGCACTTCAGCC 1321 |
| DB | 3995 | GCGACTTGCACTGCGGTATAGCTGCAATACGTTGTCAACCCAGACAGTGTGCAAGCC 4054 |
| QY | 1322 | TTGACCTTACCTTCAACATTAAGACATCAAGCTTCCCGAGGATGCTGTCCGTAATC 1381 |
| DB | 4055 | TTGACCTTACCTTCAACATTAAGACATCAAGCTTCCCGAGGATGCTGTCTCCGCACTC 4114 |
| QY | 1382 | AACTGTGGGGTATGAGCTGGCAGAGGAAAGCCAGGATCTACAGATTTGTGACCGGG 1441 |
| DB | 4115 | AACTGTGGGGCAGGACTGGCAGAGGGAAAGCCAGGATCTACAGATTTGTGACCGGG 4174 |
| QY | 1442 | AGCGTCTTCTGTGAGATTTTGACTGTGTCTCTGCGAGTGTATGACGCGGGTGTG 1501 |
| DB | 4175 | AGCGGCTCTCCGCGATGTTCAGCTGTGTCTCTGTGAGTGTATGACGAGGCTGTG 4234 |
| QY | 1502 | CTTGTATGAGCTTACGCGCGCGCGAGACCAAGTATAGGCTACAGACATATGAACACC 1561 |
| DB | 4235 | CTTGTATGAGCTTACGCGCGCGCGAGACTACAGTATAGGCTACAGAGCTATGAACACC 4294 |
| QY | 1562 | CGGACTTCCCGTGTGCAAGACCACTTTGAATTTTGGAGGGCGCTTTACGAGGTCTCA 1621 |
| DB | 4295 | CGGACTTCCCGTGTGCGAGGACCACTTTGAATTTTGGAGGGCGCTTTACGAGGCTCA 4354 |
| QY | 1622 | CCCACTATGAGCGCCCATCTTCTATCCCAAGACAAAGAGTGGGAAAACTTCCCTATC 1681 |
| DB | 4355 | CTCATATGATGTCGCCCATCTTCTATCCCAAGACAAAGAGTGGGAGAACTTCTTACC 4414 |
| QY | 1682 | TGTTAGCGTACCAAGCACCGGTGCGGTAGAGCTCAAGCGCTCCCGCGTGTGGAGCC 1741 |
| DB | 4415 | TGTTAGCGTACCAAGCACCGGTGCGGTAGAGCTCAAGCGCTCCCGCGTGTGGAGCC 4474 |
| QY | 1742 | AGATGTGAAAGTGTGATCCGCTCAAGGCCACCTCCATGGGCAACACTCTGTAT 1801 |
| DB | 4475 | AGATGTGAAAGTGTGATTCGCTCAAGGCCACCTCCATGGGCAACACTCTGTAT 4534 |
| QY | 1802 | ATGACCTGGCGCTGTCCAGAAATGAATGACCTCTGACGCAACCACTACCAAGTATATCA 1861 |
| DB | 4535 | ACAGACTGGCGCTGTCCAGAAATGAATGACCTCTGACGCAACCACTACCAAGTATATCA 4594 |
| QY | 1862 | TGACATGATATGCGGCTGACCTGAGAGTGTGACAGATGACCTGGGAGTGTGGCGGG 1921 |
| DB | 4595 | TGACATGATATGCGGCTGACCTGAGAGTGTGACAGAGCTGAGGAGTGTGGCGGG 4654 |
| QY | 1922 | TTCTGGCTCTTTGGCGCGGTATTTGCTTACCAAGGCTGCGTGTGATAGTATGAGGA 1981 |
| DB | 4655 | TTCTGGCTCTTTGGCGCGGTATTTGCTTCAACAGGCTGCGTGTGATAGTATGAGGA 4714 |
| QY | 1982 | TTGTCTTGTCCGGAAGCGCGCAATCATCCGACAGGGAAGTCTCTACCGGAGTTG 2041 |
| DB | 4715 | TGCTCTTGTCCGGAAGCGCGCAATCATCTGACAGGGAAGTCTCTACCGAGATTG 4774 |
| QY | 2042 | ATGAATGAGAGAGTGT 2059 |
| DB | 4775 | ATGAATGAGAGAGTGT 4792 |

RESULT 10

AAZ07656
ID AAZ07656 standard; DNA; 9133 BP.
XX
AC AAZ07656;
XX
DT 20-MAR-2003 (revised)
DT 08-NOV-1999 (first entry)
XX
DE Nucleotide sequence of HCV-1 ORF.
XX
KM Hepatitis C virus; HCV; J1, J7, HCV-1; non-A, non-B HCV; NANBH;
KM HCV infection; vaccine; ds.
XX
OS Hepatitis C virus.
XX
FH Key Location/Qualifiers
FT CDS 268..9132
FT /tag=b
FT /transl_except= (pos:1588..1589; aa:Leu)
FT /note= "this codon has an apparent 1 nucleotide deletion,
FT which alters the reading frame."
FT /transl_except= (pos:1647..1650; aa:Pro)
FT /note= "this codon has an apparent 1 nucleotide
FT insertion, which alters the reading frame; this insertion
FT is not indicated in the sequence present in the formal
FT sequence listing of the specification"
XX
PM EP939128-A2.
XX
PD 01-SEP-1999.
XX
PF 17-SEP-1990; 99EP-00101746.
XX
PR 15-SEP-1989; 89US-00408045.
PR 21-DEC-1989; 89US-00456142.
PR 17-SEP-1990; 90EP-00310149.
XX
PA (OVAA/) OVA A.
PA (CHTR) CHIRON CORP.
PI Miyamura T, Saito I, Houghton M, Weiner AJ, Han J, Kolberg JA;
PI Cha T, Irvine BD;
PI WPI: 1999-480843/41.
DR P-PSDB; AAY14975.
XX
PT New Hepatitis C virus isolates, useful for diagnosis of hepatitis
PT infections and development of vaccines.
XX
PS Disclosure; Fig 12; 132pp; English.
XX
CC The invention provides two new isolates of hepatitis C virus (HCV), J1
CC and J7. These two isolates comprise nucleotide and amino acid sequences
CC that are distinct from the HCV isolate HCV-1. The nucleotide sequences
CC may be used to detect non-A, non-B HCV (NANBH) polynucleotides by
CC hybridization for diagnosis of NANBH infections. They may also be used to
CC screen blood donors, donated blood and blood products for this infection.
CC The isolates may also be used to isolate other naturally occurring
CC variants of the virus. The polypeptides may be used as a vaccine for
CC administration to patients to protect against infection with NANBH. The
CC present sequence represents the nucleotide sequence of HCV-1 ORF.
CC (Updated on 20-MAR-2003 to correct PF field.) (Updated on 20-MAR-2003 to
CC correct PR field.)
XX
SQ Sequence 9133 BP; 1834 A; 2772 C; 2600 G; 1927 T; 0 U; 0 Other;
Query Match 86.7%; Score 1786; DB 2; Length 9133;
Best Local Similarity 91.7%; Pred. No. 0;
Matches 1088; Conservative 0; Mismatches 170; Indels 0; Gaps 0;
QY 2 TGGCGCTATCAAGCGCTATGCCAGACAGCAAGGGGCTTTGGAGTCATATACCA 61
DB TGGCGCTATCAAGCGCTATGCCAGACAGCAAGGGGCTTTGGAGTCATATACCA 3403

QY 62 GCTTGAACCGGCGGAGCAAAAAACGAGTGAAGGGGTTCAGATCGTCACTGCTG 121
DB GCTTGAACCGGCGGAGCAAAAAACGAGTGAAGGGGTTCAGATCGTCACTGCTG 3463
QY 122 CCCAGACTTTCTTGGCAACTGCAATTAAGGGGTGTGAGCTGTCTACATGAGCCG 181
DB CCCAGACTTTCTTGGCAACTGCAATTAAGGGGTGTGAGCTGTCTACATGAGCCG 3523
QY 182 GAACAAAGAACATTTGGCTTCACTTAAGGGTCCCTGTTATCAAGATGACCAATGAGACC 241
DB GAACAAAGAACATTTGGCTTCACTTAAGGGTCCCTGTTATCAAGATGACCAATGAGACC 3583
QY 242 AAGACCTGTAGAGCTGAGCCCGCTCCCAAGGTGCGGCTATTAAACCATGCACTTGGC 301
DB AAGACCTGTAGAGCTGAGCCCGCTCCCAAGGTGCGGCTATTAAACCATGCACTTGGC 3643
QY 302 GCTCTCTGGAACCTTTTACCTGTGTCAGAGGCAAGCGGATGTCAATTCGTGCGCGAGCGG 361
DB GCTCTCTGGAACCTTTTACCTGTGTCAGAGGCAAGCGGATGTCAATTCGTGCGCGAGCGG 3703
QY 362 GTGATGAGAGGGGCAAGCTGCTTTTGGCCCCCGGCTATCTCTTACTTGAAGGCTCCTCGG 421
DB GTGATGAGAGGGGCAAGCTGCTTTTGGCCCCCGGCTATCTCTTACTTGAAGGCTCCTCGG 3763
QY 422 GAGGCCCTGTGCTGTGCCCCCGAGGACATGCGGTAGGCAATTCAGAGCGCGGTATGCA 481
DB GAGGCCCTGTGCTGTGCCCCCGAGGACATGCGGTAGGCAATTCAGAGCGCGGTATGCA 3823
QY 482 CCCGTGAGTGGCTTAAGGCGGTGGACTTTCATCCCGTGAAGAGCTTGAAGAACCAATCA 541
DB CCCGTGAGTGGCTTAAGGCGGTGGACTTTCATCCCGTGAAGAGCTTGAAGAACCAATCA 3883
QY 3824 CCCGTGAGTGGCTTAAGGCGGTGGACTTTCATCCCGTGAAGAGCTTGAAGAACCAATCA 3883
QY 542 GGTCTCCCGGTGTCTTCAACAACTCTCTCCCAACGAGCTGCCAGAGCTTCAAGTGG 601
DB GGTCTCCCGGTGTCTTCAACAACTCTCTCCCAACGAGCTGCCAGAGCTTCAAGTGG 3943
QY 3884 GGTCTCCCGGTGTCTTCAACAACTCTCTCCCAACGAGCTGCCAGAGCTTCAAGTGG 3943
QY 602 CCCACCTGATGCTCTCCACCGGCGAGGTAAGAGCAACGAGTCCCGGCGGATGCGAG 661
DB CCCACCTGATGCTCTCCACCGGCGAGGTAAGAGCAACGAGTCCCGGCGGATGCGAG 4003
QY 3944 CTCACCTTCATGCTCTCCACGAGCGGCAAGCAAGCAAGTCCCGGCGGATGCGAG 4003
QY 662 CTCAGGGGCTTAAGGCTGTGCTCAACCCCTCGGTGCTGCAACATGAGGCTTTGGTG 721
DB CTCAGGGGCTTAAGGCTGTGCTCAACCCCTCGGTGCTGCAACATGAGGCTTTGGTG 4063
QY 722 CTTAATATGTCAGAGCCCATGAGATTGATCCCTAATCAGAGCTGAGGAGAGCAATTA 781
DB CTTAATATGTCAGAGCCCATGAGATTGATCCCTAATCAGAGCTGAGGAGAGCAATTA 4123
QY 4064 CTTAATATGTCAGAGCCCATGAGATTGATCCCTAATCAGAGCTGAGGAGAGCAATTA 4123
QY 782 CTACTGAGAGCCGATCACTGATTCACCTAAGGCAAGTTCCTTCCGAGCGGAGTGT 841
DB CTACTGAGAGCCGATCACTGATTCACCTAAGGCAAGTTCCTTCCGAGCGGAGTGT 4183
QY 4124 CCACTGAGAGCCGATCACTGATTCACCTAAGGCAAGTTCCTTCCGAGCGGAGTGT 4183
QY 842 CAGGGGAGCTTATGATCAATTAATTTTGAAGTGCATCCAGATGCAATTCGA 901
DB CAGGGGAGCTTATGATCAATTAATTTTGAAGTGCATCCAGATGCAATTCGA 4243
QY 4184 CAGGGGAGCTTATGATCAATTAATTTTGAAGTGCATCCAGATGCAATTCGA 4243
QY 902 TCTTGGGATGAGCACTGTCTTGAACCAAGAGAACCGCGGGGCGAGACTGATCTGTC 961
DB TCTTGGGATGAGCACTGTCTTGAACCAAGAGAACCGCGGGGCGAGACTGATCTGTC 4303
QY 4244 TCTTGGGATGAGCACTGTCTTGAACCAAGAGAACCGCGGGGCGAGACTGATCTGTC 961
DB TCTTGGGATGAGCACTGTCTTGAACCAAGAGAACCGCGGGGCGAGACTGATCTGTC 4363
QY 962 TCGCCAGGCTAAGCCCTCGGGCTCGTCACTGTGCCCATCTTAACATGAGAGTGG 1021
DB TCGCCAGGCTAAGCCCTCGGGCTCGTCACTGTGCCCATCTTAACATGAGAGTGG 4363
QY 4304 TCGCCAGGCTAAGCCCTCGGGCTCGTCACTGTGCCCATCTTAACATGAGAGTGG 4363
QY 1022 CTCTGTGCACTAAGCGAGAGATCCCTTTTATGAGAGGCTATTCCTTGAAGCAATTA 1081
DB CTCTGTGCACTAAGCGAGAGATCCCTTTTATGAGAGGCTATTCCTTGAAGCAATTA 4423
QY 4364 CTCTGTGCACTAAGCGAGAGATCCCTTTTATGAGAGGCTATTCCTTGAAGCAATTA 4423
QY 1082 AGGGGGGAGACATTTCTATCTTGGCACTGAAGAGAGGAGAGAGTCTGCGCGAA 1141
DB AGGGGGGAGACATTTCTATCTTGGCACTGAAGAGAGGAGAGTCTGCGCGAA 4483
QY 4424 AGGGGGGAGACATTTCTATCTTGGCACTGAAGAGAGGAGAGTCTGCGCGAA 4483

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QY 1142 AACTGTCGCGTGGGCGCTGAATGCCGTGGCTTAACACCGCGGCTTGATGTGCTGCA 1201
DB 4484 AGCTGTGCGCATTTGGGCAATCAATGCCGTGGCTTAACACCGCGGCTTGATGTGCTGCA 4543
QY 1202 TCCCGACCAAGTGTGAAGTGTGCTGCTGCTGCAATGACCGCTCATGACCGGCTTTACCG 1261
DB 4544 TCCCGACCAAGTGTGAAGTGTGCTGCTGCTGCAATGACCGCTCATGACCGGCTTTACCG 4603
QY 1262 GGGACTTGATTCGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1321
DB 4604 GGGACTTGATTCGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4663
QY 1322 TTGACCCCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCT 1381
DB 4664 TTGACCCCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCT 4723
QY 1382 AACGTCGGGGATGAGACTGGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1441
DB 4724 AACGTCGGGGATGAGACTGGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4783
QY 1442 AGCGTCCTTCTGCGATGTTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1501
DB 4784 AGCGTCCTTCTGCGATGTTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4843
QY 1502 CTTGGTATGAGCTTACGCGCGCGCGAGAGCAGAGTATGAGCTTACGAGCTATGAGAAACACC 1561
DB 4844 CTTGGTATGAGCTTACGCGCGCGCGAGAGCAGAGTATGAGCTTACGAGCTATGAGAAACACC 4903
QY 1562 CGGGACCTTCCGCTGTCGCAAGACCATCTTGAAATTTTGGAGGCGCTTTTACGCGGCTTCA 1621
DB 4904 CGGGACCTTCCGCTGTCGCAAGACCATCTTGAAATTTTGGAGGCGCTTTTACGCGGCTTCA 4963
QY 1622 CCCACATGAGCGCCCACTTCTTATCCCAAGACCAAGAGTGGGAGAAAACCTTCCCTATC 1681
DB 4964 CTCATATGATGATCCCACTTCTTATCCCAAGACCAAGAGTGGGAGAAAACCTTCCCTATC 5023
QY 1682 TGGTAGCGTACCAAGCAGCAGTGTGCGCTAGAGCTCAAGCCCTCCCGTGTGGAGACC 1741
DB 5024 TGGTAGCGTACCAAGCAGCAGTGTGCGCTAGAGCTCAAGCCCTCCCGTGTGGAGACC 5083
QY 1742 AGATGTGAGAGTGTGATCGTCTTCAAGCCCACTTCCAGTGGGCGCAACCTTGTCTAT 1801
DB 5084 AGATGTGAGAGTGTGATCGTCTTCAAGCCCACTTCCAGTGGGCGCAACCTTGTCTAT 5143
QY 1802 ATAGACTGGGCGCTGTGCAAGATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAA 1861
DB 5144 ATAGACTGGGCGCTGTGCAAGATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAA 5203
QY 1862 TGAACATGATGTGCGGCTGACCTGGAAGTGTGACGAGTACCTGCGGTGCTGTTGGCGGCG 1921
DB 5204 TGAACATGATGTGCGGCTGACCTGGAAGTGTGACGAGTACCTGCGGTGCTGTTGGCGGCG 5263
QY 1922 TTCTGCGCTGCTTGGCGCGGCTATTTGCTATTCACAGGCTGCGGTGCTATGATGATGAGA 1981
DB 5264 TTCTGCGCTGCTTGGCGCGGCTATTTGCTATTCACAGGCTGCGGTGCTATGATGATGAGA 5323
QY 1982 TTGCTCTTGTCCGGAAGCCGCGCATATACCGGAGAGTCTCTTACCGGAGTTTG 2041
DB 5324 TTGCTCTTGTCCGGAAGCCGCGCATATACCGGAGAGTCTCTTACCGGAGTTTG 5383
QY 2042 ATGAATGAGAGAGTGTCT 2059
DB 5384 ATGAATGAGAGAGTGTCT 5401
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XX Hepatitis C virus strain 1 DNA.
DE
XX Hepatitis C virus; HCV-1; non-A, non-B hepatitis; HCV antigen;
KM viral infections; ss.
XX
OS Hepatitis C virus.
XX
PN EP14475-A.
PD
XX 27-FEB-1991.
PF
XX 21-AUG-1990; 90BP-00309120.
PR
XX 25-AUG-1989; 89US-00398667.
XX
PA (CHIR ) CHIRON CORP.
PI
XX Weiner AJ, Steimer KS;
XX
DR WPI; 1991-059670/09.
XX
PT Cell lines infected with hepatitis C virus - are used as source of
PT antigens for detection of HCV antibodies, for vaccines, and for screening
PT anti-viral agents.
PS
XX Disclosure; Fig 1; 24pp; English.
XX
XX This is a hepatitis C virus (HCV) composite cDNA sequence, deduced using
CC overlapping clones, a compsn. contg. the antigenic protein encoded by
CC this sequence is useful for detecting anti-HCV anti- bodies (Abs) and for
CC screening an agent which inhibits HCV replic- ation. A cell line infected
CC with this virus can be used as a source of antigens. The antigen is
CC useful for preparing vaccines for treating viral infections. See also
CC AAQ10567. (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 9185 BP; 1849 A; 2790 C; 2608 G; 1938 T; 0 U; 0 Other;
XX
Query Match 86.7%; Score 1786; DB 2; Length 9185;
Best Local Similarity 91.7%; Pred. No. 0;
Matches 1888; Conservative 0; Mismatches 170; Indels 0; Gaps 0;
QY 2 TGGCGCTATACAGCGCTATGCGCAGACAGAGGCGCTTTGGAGTGCATATACCA 61
DB 3396 TGGCGCTATACAGCGCTATGCGCAGACAGAGGCGCTTTGGAGTGCATATACCA 3455
QY 62 GCTTACCGCGCGGAGCAAAAACAAGTGAAGGTTGAGTGCATGCTGCACTGCTG 121
DB 3456 GCTTACCGCGCGGAGCAAAAACAAGTGAAGGTTGAGTGCATGCTGCACTGCTG 3515
QY 122 CCCAAGCTTCTTGGCAACCTGCAATTAAGGGGTGTGATGCTGCTTACATGAGCCG 181
DB 3516 CCCAAGCTTCTTGGCAACCTGCAATTAAGGGGTGTGATGCTGCTTACATGAGCCG 3575
QY 182 GAAAGAGACATGCGTACCTTAAGGCTCTGTTATCCAGATGTAACCAATGTGAGCC 241
DB 3576 GAAAGAGACATGCGTACCTTAAGGCTCTGTTATCCAGATGTAACCAATGTGAGCC 3635
QY 3576 GAAAGAGACATGCGTACCTTAAGGCTCTGTTATCCAGATGTAACCAATGTGAGCC 3635
QY 242 AAGACTGTGAGTGTGCGCGCTGCGCTCCCAAGTGTGCGCTCATTAACCACTGCTG 301
DB 3636 AAGACTGTGAGTGTGCGCGCTGCGCTCCCAAGTGTGCGCTCATTAACCACTGCTG 3695
QY 302 GCTCTCTGGAAGCTTTAAGTGTGCAAGAGGCAAGCGGATGATTTCTGTGCGCGGAG 361
DB 3696 GCTCTCTGGAAGCTTTAAGTGTGCAAGAGGCAAGCGGATGATTTCTGTGCGCGGAG 3755
QY 362 GTGATGAGAGGCGAGCTGTTTGGCGCGGCTATCTTACTTGAAGGCTCTCTCG 421
DB 3756 GTGATGAGAGGCGAGCTGTTTGGCGCGGCTATCTTACTTGAAGGCTCTCTCG 3815
QY 422 GAGGCCCTTCTGTGCGCGCGGAGACATGCGTGAAGCATATTCAGAGCGCGGTATGCA 481
DB 3816 GAGGCCCTTCTGTGCGCGCGGAGACATGCGTGAAGCATATTCAGAGCGCGGTATGCA 3875
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QY 482 CCCGTTGAGTGAAGGCGGTGGACTTCAATCCCGTGAAGAGCTTGAAGACAACCATGA 541
 Db 3876 CCCGTTGAGTGAAGGCGGTGGACTTCAATCCCGTGAAGAGCTTGAAGACAACCATGA 3935
 QY 542 GGTCCCGGTGTTCTCAGACAACCTCTCCCAACAGCAAGTGCCTCAGAGCTTCAAGTGG 601
 Db 3936 GGTCCCGGTGTTCAAGATTAACCTCTCCCAACAGTATGCCCCAGAGCTTCAAGTGG 3995
 QY 602 CCCAGCTGATGCTCCCAACCGGCAAGGTGAAGACAACCAAGTCCCGGCGCATACGAG 661
 Db 3996 CTCACCTTCATGCTCCCAACAGGCAAGGCAAAAGCAACCAAGTCCCGGCGCATATGCA 4055
 QY 662 CTCAGGCGCTAAGAGGTGCTGCTCAACCCCTCCGTTGCTGCAACAATGAGGCTTTGGT 721
 Db 4056 CTCAGGCGCTAAGAGGTGCTGCTCAACCCCTCTGTTGCTGCAACACTGAGCTTTGGT 4115
 QY 722 CTTAACATGTCAGAGGCCCATGGGATTTGATCTTAACATCAGAGCTGGGATGAAGACAATTA 781
 Db 4116 CTTAACATGTCAGAGGCCCATGGGATTTGATCTTAACATCAGAGCTGGGATGAAGACAATTA 4175
 QY 782 CTACTGCGAGCCCGATCAGATATTCACCTACGCAAGTTCCTTGGCCGCGGCTTT 841
 Db 4176 CCACCTGCGAGCCCGATCAGATATTCACCTACGCAAGTTCCTTGGCCGCGGCTTT 4235
 QY 842 CAGGGGGTCTTATGACATATTAATTGTCAGAGTGCACCTCAAGATGCAACATCA 901
 Db 4236 CCGGGGGCGCTTATGACATATTAATTGTCAGAGTGCACCTCAAGATGCAACATCA 4295
 QY 902 TCTTGGGCAATTGGCACTGTCCTTGAACAGAGAGACCGGGGGGCGAGACTGACTGTC 961
 Db 4296 TCTTGGGCAATTGGCACTGTCCTTGAACAGAGAGACCGGGGGGCGAGACTGACTGTC 4355
 QY 962 TGGCCACCGCTACCCCTCCGGGCTCGGTCACTGTGCCCCATCTTAACATCGAGAGTGG 1021
 Db 4356 TGGCCACCGCTACCCCTCCGGGCTCGGTCACTGTGCCCCATCTTAACATCGAGAGTGG 4415
 QY 1022 CTCTGTCACCTACCGGAGAGATCCCTTTTATGGCAAGGCTATTCCTCTGAAGCAATTA 1081
 Db 4416 CTCTGTCACCTACCGGAGAGATCCCTTTTATGGCAAGGCTATTCCTCTGAAGCAATTA 4475
 QY 1082 AGGGGGGAGAGATCTCATCTTCTGCACTCAAGAGAGAGTGCAGAGCTCGCGCA 1141
 Db 4476 AGGGGGGAGAGATCTCATCTTCTGCACTCAAGAGAGAGTGCAGAGCTCGCGCA 4535
 QY 1142 AACTGTGCGGTTGGGCGCTCAATGCGGTGCTTAACACCGGCGCTTGAATGTGCCGTCA 1201
 Db 4536 AACTGTGCGGTTGGGCGCTCAATGCGGTGCTTAACACCGGCGCTTGAATGTGCCGTCA 4595
 QY 1202 TCCCGACAGTGTGACGTTGTGCTGTGAGCAATGACGCGCTCATGACCGGCTTTACCG 1261
 Db 4596 TCCCGACAGTGTGACGTTGTGCTGTGAGCAATGACGCGCTCATGACCGGCTTTACCG 4655
 QY 1262 GCGACTCTGATTCGATGATGACTGCAACAGTGTGCAACCGACAGTGCATTCAGCC 1321
 Db 4656 GCGACTCTGATTCGATGATGACTGCAACAGTGTGCAACCGACAGTGCATTCAGCC 4715
 QY 1322 TTGACCTTACCTTACCATTTGAGACAATACGCTTCCCAAGATGTGTCTCCCGATCTC 1381
 Db 4716 TTGACCTTACCTTACCATTTGAGACAATACGCTTCCCAAGATGTGTCTCCCGATCTC 4775
 QY 1382 AACGTGGGGTGAAGACTGCGAGAGGAGCAGGACATCTAAGATTGTTGGACCGGGGG 1441
 Db 4776 AACGTGGGGTGAAGACTGCGAGAGGAGCAGGACATCTAAGATTGTTGGACCGGGGG 4835
 QY 1442 AGCGTCTCTTCTGAGCATGTTGACTGCTGTCTCTGCGAGTGTCTAAGACGCGGTTGGT 1501
 Db 4836 AGCGTCTCTTCTGAGCATGTTGACTGCTGTCTCTGCGAGTGTCTAAGACGCGGTTGGT 4895
 QY 1502 CTTGGTATAGCTTACGCGCGCGCGAGACCAACGTTAGGCTTGAAGATCAATGAACACC 1561
 Db 4896 CTTGGTATAGCTTACGCGCGCGCGAGACCAACGTTAGGCTTGAAGATCAATGAACACC 4955

QY 1562 CGGACCTCCCGTGTGCCAAGACCATCTTGAATTTTGGAGGGCGTCTTACCGGCTCA 1621
 Db 4956 CGGACCTCCCGTGTGCCAAGACCATCTTGAATTTTGGAGGGCGTCTTACCGGCTCA 5015
 QY 1622 CCCACATGAGCGCCCATCTTCTATCCAGACACAGATGTTGGGAAAACTTCCCTATC 1681
 Db 5016 CTCATATGATGCGCCCATCTTCTATCCAGACACAGATGTTGGGAAAACTTCCCTATC 5075
 QY 1682 TGTGACCTTACCAACCGCGTGTGCTAGAGCTCAAGCCCTCCCGGCGTGGGAGC 1741
 Db 5076 TGTGACCTTACCAACCGCGTGTGCTAGAGCTCAAGCCCTCCCGGCGTGGGAGC 5135
 QY 1742 AGATGTGAAGTGTCTGATTCGCTCAAGCCCATCTCATAGGCGCAACCTCTGCTAT 1801
 Db 5136 AGATGTGAAGTGTCTGATTCGCTCAAGCCCATCTCATAGGCGCAACCTCTGCTAT 5195
 QY 1802 ATGACTGCGCGCTGTCCAGAAATGAATGACCTTGAACGACCTCAGTACCAATATATCA 1861
 Db 5196 ACAGACTGCGCGCTGTCCAGAAATGAATGACCTTGAACGACCTCAGTACCAATATATCA 5255
 QY 1862 TGACATGATGTGCGGCTGACCTGAGAGTGTGTCAGAGTACCTGGGAGCTGTTGGCGGC 1921
 Db 5256 TGACATGATGTGCGGCTGACCTGAGAGTGTGTCAGAGTACCTGGGAGCTGTTGGCGGC 5315
 QY 1922 TTCTGCTGCTTTGGCGCGATTTGCTATCCACAGGCTGCGTGTCTATAGTATGAGA 1981
 Db 5316 TTCTGCTGCTTTGGCGCGATTTGCTATCCACAGGCTGCGTGTCTATAGTATGAGA 5375
 QY 1982 TTGTCTTGTCCGGAAGCCGCGCATCATACCGACAGGGAAGTCTCTACCGGAGTTGG 2041
 Db 5376 TTGTCTTGTCCGGAAGCCGCGCATCATACCGACAGGGAAGTCTCTACCGGAGTTGG 5435
 QY 2042 ATGAATGAAGAGTGTCT 2059
 Db 5436 ATGAATGAAGAGTGTCT 5453

RESULT 12
 AAA75297
 ID AAA75297 standard; cDNA, 9185 BP.
 XX
 AC AAA75297;
 XX
 DT 15-JAN-2001 (first entry)
 XX
 DE Sense strand of HCV encoding a polyprotein.
 XX
 KW Hepatitis C virus; HCV; antisense polynucleotide; polyprotein;
 KW viral infectivity; viral replication; ds.
 OS Hepatitis C virus.
 XX
 FT Key
 FT CDS Location/Qualifiers
 FT 320..9184
 FT /*tag= a
 FT /note= "partial sequence; no termination codon given"
 XX
 PN EP1034785-A2.
 PD 13-SEP-2000.
 XX
 PF 16-MAR-1990; 2000BP--00109602.
 XX
 PR 17-MAR-1989; 89US-00325338.
 PR 20-APR-1989; 89US-00341334.
 PR 18-MAY-1989; 89US-00355002.
 PR 16-MAR-1990; 90BP-00302866.
 XX
 XX (CHTR) CHIRON CORP.
 XX
 XX Houghton M, Choo Q, Kuo G;
 FI
 XX WPI; 2000-566891/53.

DR P-PSDB; AAB18541.

XX Novel composition comprising a hepatitis C virus antisense polynucleotide
PT which is complementary to or corresponds to a sense strand of the virus
PT genome, and selectively hybridizes to it.

XX Example; Fig 17; 75pp; English.

XX The specification describes a pharmaceutical composition which comprises
CC a hepatitis C virus (HCV) antisense polynucleotide. The HCV is
CC characterized by a positive stranded RNA genome which has 40% homology at
CC the polypeptide level to a HCV polypeptide. The antisense polynucleotide
CC binds to cellular polynucleotides which enhance and/or are required for
CC viral infectivity, replicative ability or chronicity. The antisense
CC polynucleotides may also be designed to bind with high specificity, to be
CC of increased stability, to be stable and to have low toxicity. The
CC composition also comprises an agent which causes viral RNA to be
CC inactive. The composition is used for preventing HCV replication in a
CC system. The present sequence represents a novel HCV cDNA sequence, which
CC is used in the course of the invention

XX Sequence 9185 BP; 1849 A; 2790 C; 2608 G; 1938 T; 0 U; 0 Other;

Query Match 86.7%; Score 1786; DB 3; Length 9185;
Best Local Similarity 91.7%; Pred. No. 0;
Matches 1088; Conservative 0; Mismatches 170; Indels 0; Gaps 0;

QY 2 TGGCCGCTATCAAGCGCTATGCCAGACAGCAAGGGGCTTTGGAGTCATATCCCA 61
DB 3396 TGGCCGCTATCAAGCGCTATGCCAGACAGCAAGGGGCTTTGGAGTCATATCCCA 3455
QY 62 GCTTGAACCGCGCGGACAAACACAGTGAAGGTGAAGTTGATCGTGAACCTGCTG 121
DB 3456 GCTTGAACCGCGCGGACAAACACAGTGAAGGTGAAGTTGATCGTGAACCTGCTG 3515
QY 122 CCACAGCTTTCTTGGACACCTGCAATTAACGGGGTGTGTGACCTGTCTACATGAGCCG 181
DB 3516 CCACAGCTTTCTTGGACACCTGCAATTAACGGGGTGTGTGACCTGTCTACATGAGCCG 3575
QY 182 GAACAGAGCAATGGCTGACCTAAGAGGTCTGTTATCCAGATGTAACCAATGTGAGAC 241
DB 3576 GAACAGAGCAATGGCTGACCTAAGAGGTCTGTTATCCAGATGTAACCAATGTGAGAC 3635
QY 242 AAGACTCTGTAAGCTGAGCGCGCTCCCAAGTGCCTGCTATTAACACATGCACTTGG 301
DB 3636 AAGACTCTGTAAGCTGAGCGCGCTCCCAAGTGCCTGCTATTAACACATGCACTTGG 3695
QY 302 GCTCTCGGACCTTTAAGCTGTCAAGAGGACGCGAGTCAATTCCTGTGCGCCGACGG 361
DB 3696 GCTCTCGGACCTTTAAGCTGTCAAGAGGACGCGAGTCAATTCCTGTGCGCCGACGG 3755
QY 362 GTGATGACAGGGGACGCGCTGTTGCGCCCGGCTATCTCTTAAGTAAAGCTCTCTCG 421
DB 3756 GTGATGACAGGGGACGCGCTGTTGCGCCCGGCTATCTCTTAAGTAAAGCTCTCTCG 3815
QY 422 GAGGCGCTTGTCTGTGCCCCGACAGACATGCGGTAGGCATTTACAGAGCGCGGTATGA 481
DB 3816 GAGGCGCTTGTCTGTGCCCCGACAGACATGCGGTAGGCATTTATTAAGGCGCGGTATGA 3875
QY 482 CCCGTAAGTGAAGTGAAGGGGAGTGAATTCATCCCCGTAGAGACTTGAAGACCAATGA 541
DB 3876 CCCGTAAGTGAAGTGAAGGGGAGTGAATTCATCCCCGTAGAGACTTGAAGACCAATGA 3935
QY 542 GGTCCCGGCTGTTCTACAGCAATCTCTCCCAACAGACAGTGCCTCCAGACTTCAAGTGG 601
DB 3936 GGTCCCGGCTGTTCTACAGCAATCTCTCCCAACAGACAGTGCCTCCAGACTTCAAGTGG 3995
QY 602 CCCACTGTGATGCTCCACCGGACAGGTGAAGACCAAGTCCCGGCGCATATAGCGAG 661
DB 3996 CCCACTGTGATGCTCCACCGGACAGGTGAAGACCAAGTCCCGGCGCATATAGCGAG 4055
QY 662 CTCAGGGCTTAAGAGTGTGTGCTCAACCCCTCGTTGCTGCAACATAGGGCTTTGGTG 721
DB 721 CTCAGGGCTTAAGAGTGTGTGCTCAACCCCTCGTTGCTGCAACATAGGGCTTTGGTG

DB 4056 CTCAGGGCTTAAGAGTGTGTGCTCAACCCCTCGTTGCTGCAACATAGGGCTTTGGTG 4115
QY 722 CTATAGTGTCAAGGCGCATGGGATTTGATTCCTAATCAAGACATGGGGTGAAGACAATTA 761
DB 4116 CTATAGTGTCAAGGCGCATGGGATTTGATTCCTAATCAAGACATGGGGTGAAGACAATTA 4175
QY 782 CTACTGAGAGCCGATCAAGTATTCACCTACGGAAGTTCCTTCCGACGCGGGTGT 841
DB 4176 CCACGTGAGAGCCGATCAAGTATTCACCTACGGAAGTTCCTTCCGACGCGGGTGT 4235
QY 842 CAGGGGCTTATGACATATATTTGTGACAGTGCATCTCCAGATGCAATCCA 901
DB 4236 CAGGGGCTTATGACATATATTTGTGACAGTGCATCTCCAGATGCAATCCA 4295
QY 902 TCTTGGGATTTGGACATGCTGCTTGAACAGACAGACCGCGGGGCGAGACTGATGTGC 961
DB 4296 TCTTGGGATTTGGACATGCTGCTTGAACAGACAGACCGCGGGGCGAGACTGATGTGC 4355
QY 962 TGGCCAGCGTACCCCTCGGGCTCCGTACATGTGCCCATCTTAACATCGAGAGTTTG 1021
DB 4356 TGGCCAGCGTACCCCTCGGGCTCCGTACATGTGCCCATCTTAACATCGAGAGTTTG 4415
QY 1022 CTGTGTCACTACCGAGAGATCCCTTTTATGCAAGGCTATTCCTTGAACCAATTA 1081
DB 4416 CTGTGTCACTACCGAGAGATCCCTTTTATGCAAGGCTATTCCTTGAACCAATTA 4475
QY 1082 AAGGGGAGAGACATCTCATCTTCTGCACTCAAAAGAAAGTGCACAGCTCGCGCA 1141
DB 4476 AAGGGGAGAGACATCTCATCTTCTGCACTCAAAAGAAAGTGCACAGCTCGCGCA 4535
QY 1142 AACTGTGCGCTTGGGCGTCAATGCGGTGCTTACACCGCGGCTTGAATGTGCTGTA 1201
DB 4536 AACTGTGCGCTTGGGCGTCAATGCGGTGCTTACACCGCGGCTTGAATGTGCTGTA 4595
QY 1202 TCCGACCAAGTGTGACGTTGTCTGTGTGACCAATGACGCGCTCATGACGCGCTTTAC 1261
DB 4596 TCCGACCAAGTGTGACGTTGTGTGTGACCAATGACGCGCTCATGACGCGCTTTAC 4655
QY 1262 GCGACTTGGATTCGTTGATGACCTGCAACACCTGTGTACCCAGACATGCACTTCAAGC 1321
DB 4656 GCGACTTGGATTCGTTGATGACCTGCAACACCTGTGTACCCAGACATGCACTTCAAGC 4715
QY 1322 TTGACCTTACCTTACATGATGACCAATCAAGCTTCCCAAGATCTGCTCCGATCTC 1381
DB 4716 TTGACCTTACCTTACATGATGACCAATCAAGCTTCCCAAGATCTGCTCCGATCTC 4775
QY 1382 AAGCTGCGGAGTGAAGCTGACAGAGGAAAGCAGGATCTACAGATTTGTGACCGGG 1441
DB 4776 AAGCTGCGGAGTGAAGCTGACAGAGGAAAGCAGGATCTACAGATTTGTGACCGGG 4835
QY 1442 AGCGTCTTCTGAGCATGTTTGAATCTGTCTCTGCGAGTGTATGACGCGGGTTGTG 1501
DB 4836 AGCGTCTTCTGAGCATGTTTGAATCTGTCTCTGCGAGTGTATGACGCGGGTTGTG 4895
QY 1502 CTTGGTATGAGCTTACGCGCGCGAGACCAAGTAAAGGCTAGAGATTAAGAACACCC 1561
DB 4896 CTTGGTATGAGCTTACGCGCGCGAGACCAAGTAAAGGCTAGAGATTAAGAACACCC 4955
QY 1562 CGGACCTTCCGCTGTGACCAAGACATCTTGAATTTTGGAGGGCGTCTTACAGGGTCTCA 1621
DB 4956 CGGACCTTCCGCTGTGACCAAGACATCTTGAATTTTGGAGGGCGTCTTACAGGGTCTCA 5015
QY 1622 CCACATGACGCGCATCTTCTATTCACAGACAAAGACAGTGGGAAAACTTCCCTATC 1681
DB 5016 CCACATGACGCGCATCTTCTATTCACAGACAAAGACAGTGGGAAAACTTCCCTATC 5075
QY 1682 TGGTACGTAACCAAGACACCGGTGCGGTAGAGCTCAAGCCCTCCCGCTGTGGAGAC 1741
DB 5076 TGGTACGTAACCAAGACACCGGTGCGGTAGAGCTCAAGCCCTCCCGCTGTGGAGAC 5135
QY 1742 AGATGTGAAGTGTCTTATCCGTCTCAAGCCCATCTTCATGGGCAACCTCTGTAT 1801
DB 5136 AGATGTGAAGTGTCTTATCCGTCTCAAGCCCATCTTCATGGGCAACCTCTGTAT 5195

QY 1802 ATAGACTGGGGCTGCTCCAGATGAAGTACCCCTGACGACCCGATCAACCAATATATCA 1861
DB 5186 ACAGACTGGGGCTGCTTTCAGATGAATATACCTTGACGACCCAGTCAACCAATATATCA 5255
QY 1862 TGACATGATATGTCGGCTGACCTGAGAGTGTGTCAGAGTACCTGGGTGCTGTTGGCGGG 1921
DB 5256 TGACATGATATGTCGGCGGACCTGAGAGTGTGTCAGAGTACCTGGGTGCTGTTGGCGGG 5315
QY 1922 TTCTGGCTGCTTTGGCGCGGCTATTTGCTTATCCAGAGCTGCTGGTCAATGATGATGA 1981
DB 5316 TCCTGGCTGCTTTGGCGCGGCTATTTGCTTATCCAGAGCTGCTGGTCAATGATGATGA 5375
QY 1982 TTGCTGTCGCGGAAAGCCGCAATGATACCGGACAGGAGTCTCTACCGGAGTTTG 2041
DB 5376 TCGTCTGTCGCGGAAAGCCGCAATGATACCTGACAGGAGTCTCTACCGAGAGTTTG 5435
QY 2042 ATGAATGGAAGATGCT 2059
DB 5436 ATGAGATGGAAGATGCT 5453

RESULT 13
ADN35979
ID ADN35979 standard; cDNA; 9185 BP.

AC ADN35979;

DT 17-JUN-2004 (first entry)

DE HCV cDNA clone #2.

KM Antiviral; Vaccine; hepatitis C virus infection; HCV infection; ss.

OS Hepatitis C virus.

PN EPI394255-A2.

PD 03-MAR-2004.

PF 16-MAR-1990; 2003BP-00016585.

PR 17-MAR-1989; 89US-00325338.

PR 20-APR-1989; 89US-00341334.

PR 18-MAY-1989; 89US-00355002.

PR 16-MAR-1990; 90EP-00302866.

PA (CHIR) CHIRON CORP.

PI Houghton M, Choo Q, Kuo G;

DR WPI; 2004-193149/19.

DR P-PSDB; ADN35978.

PT Novel purified hepatitis C virus polypeptide comprising epitope encoded

PT by hepatitis C virus cDNA, useful as vaccine for treating hepatitis C

PT virus.

PS Claim 1; Fig 17; 79PD; English.

CC The present invention relates to hepatitis C virus (HCV) proteins and

CC cDNA sequences. The sequences are useful in immunoassays for detecting

CC antibodies directed against HCV antigen; preparing host cells transformed

CC with a recombinant polynucleotide; screening antiviral agents and

CC determining the effect of antiviral agent in inhibiting viral replication

CC in cell culture system; and developing vaccine for treating HCV

CC infection.

XX Sequence 9185 BP; 1849 A; 2790 C; 2608 G; 1938 T; 0 U; 0 Other;

XX Query Match 86.7%; Score 1786; DB 12; Length 9185;

XX Best Local Similarity 91.7%; Pred. No. 0;

XX Matches 1888; Conservative 0; Mismatches 170; Indels 0; Gaps 0;

QY 2 TGGGCTTATCAGGCTATGCTCCAGAGACAGAAAGGGCTTTTGGAGTGCATATATCA 61
DB 3386 TGGGCTTATCAGGCTATGCTCCAGAGACAGAAAGGGCTTTTGGAGTGCATATATCA 3455
QY 62 GCTTACCGGCGGAGCAAAAAACAGGTGAGGGTTCAGATTCGTGTCACTGCTG 121
DB 3456 GCTTACCGGCGGAGCAAAAAACAGGTGAGGGTTCAGATTCGTGTCACTGCTG 3515
QY 122 CCCAGACTTTTGTGGCAACCTGCATTAACGGGGTGTGTGACTGTCTACATGAGCCG 181
DB 3516 CCCAGACTTTTGTGGCAACCTGCATTAACGGGGTGTGTGACTGTCTACATGAGCCG 3575
QY 182 GAACAAAGACCAATTCGTCACCTTAAGGGTCTGTTATCCAGATGTAACCAATGAGAAC 241
DB 3576 GAACAAAGACCAATTCGTCACCTTAAGGGTCTGTTATCCAGATGTAACCAATGAGAAC 3635
QY 242 AAGACTGTAGGCTGAGCCGCTCCCAAGGTGCCGCTCATTTAACACCATGCACTTGG 301
DB 3636 AAGACTGTAGGCTGAGCCGCTCCCAAGGTGCCGCTCATTTAACACCATGCACTTGG 3695
QY 302 GCTCTCGGACCTTTTACCTGTCACAGAGGACGCGGATGCTTCTGTGCGCCGACGGG 361
DB 3696 GCTCTCGGACCTTTTACCTGTCACAGAGGACGCGGATGCTTCTGTGCGCCGACGGG 3755
QY 362 GTGATGAGAGGGGACGCTGCTTGGCCCGGCTATCTCTTAATGAAAGGCTCCTCGG 421
DB 3756 GTGATGAGAGGGGACGCTGCTTGGCCCGGCTATCTCTTAATGAAAGGCTCCTCGG 3815
QY 422 GAGGCCCTGTGCTGTGCCCCGAGGACATGCCGATATTCAGAGCCGCGATGCA 481
DB 3816 GAGGCCCTGTGCTGTGCCCCGAGGACATGCCGATATTCAGAGCCGCGATGCA 3875
QY 482 CCCGTGAGTGGCTTAAGGCGGTGACTTATCTCCGTGAGAGGCTTAAGAGACCAATCA 541
DB 3876 CCCGTGAGTGGCTTAAGGCGGTGACTTATCTCCGTGAGAGGCTTAAGAGACCAATCA 3935
QY 542 GGTCCCGGATGTTTCAGACCACTCTCCGACAGAGTGGCCGACGATCAAGTGG 601
DB 3936 GGTCCCGGATGTTTCAGACCACTCTCTCTCCAGAGTGGCCGACGATCAAGTGG 3995
QY 602 CCCACTGATGCTTCCACCGGACGCGGTAAAGAGCAAGGTCCCGCGGATACGAG 661
DB 3996 CCCACTGATGCTTCCACCGGACGCGGTAAAGAGCAAGGTCCCGCGGATACGAG 4055
QY 662 CTCAGGGCTTAAGGCTGTGCTCAACCCCTCGGTGCTGCAACAAAGGCTTTGGT 721
DB 4056 CTCAGGGCTTAAGGCTGTGCTCAACCCCTCGGTGCTGCAACAAAGGCTTTGGT 4115
QY 722 CTTACATGTCAGAGGCCCATGGGATTTGATCTTAATCATGAGAGCTGGGGTGAACAATTA 781
DB 4116 CTTACATGTCAGAGGCCCATGGGATTTGATCTTAATCATGAGAGCTGGGGTGAACAATTA 4175
QY 782 CTTACTGAGACCCGATCAAGTATTCACCTACGGAAGTTCCTTCCGACGGCGGTGT 841
DB 4176 CTTACTGAGACCCGATCAAGTATTCACCTACGGAAGTTCCTTCCGACGGCGGTGT 4235
QY 842 CAGGGGGTCTTATATATTAATTTGTGAGAGTGCACCTCCAGATGCAATCA 901
DB 4236 CAGGGGGTCTTATATATTAATTTGTGAGAGTGCACCTCCAGATGCAATCA 4295
QY 902 TCTTGGGATTTGGACCTGCTTGGACAGAGACCGCGGGGCGAGACTGACTGTGC 961
DB 4296 TCTTGGGATTTGGACCTGCTTGGACAGAGACTGCGGGGCGAGACTGACTGTGC 4355
QY 962 TCGCACCGCTAACCCCTCGGCTCGTCACTGTCGCCCATCTTAACATGAGAGTTG 1021
DB 4356 TCGCACCGCTAACCCCTCGGCTCGTCACTGTCGCCCATCTTAACATGAGAGTTG 4415
QY 1022 CTCTGTCCACTACCGGAGAGATCCCTTTTATGAGCAAGGCTATTCCTTTGAAGCAATTA 1081
DB 4416 CTCTGTCCACTACCGGAGAGATCCCTTTTATGAGCAAGGCTATTCCTTTGAAGCAATTA 4475

| | | | |
|----|------|--|-------|
| Qy | 1082 | AGGGGGGGAGACATCTCATCTCTTGCCCACTCAAAAGAAAGATGGGAGCAGCTCGCCGCA | 11411 |
| Db | 4476 | AGGGGGGGAGACATCTCATCTCTTGCTCATTTCAAAAGAAAGATGGGAGCAACTCGCCGCA | 45355 |
| Qy | 1142 | AACCTGTCGCGTTGGGCGCTCAATGCGCGCTTACTACCGCGGCGTTGATGTCCTGCA | 1201 |
| Db | 4536 | AGCTGTCGCAATTGGGCGATCAATGCGCGCTACTACCGCGGCTTGAAGTCCTGCA | 45955 |
| Qy | 1202 | TCCCGACCAAGTGTGAAGCTTGTGCTCGTGGCACTGACGCGCTTATGACCGCTTTACCG | 1261 |
| Db | 4596 | TCCCGACCAAGGGGGAGTGTGTGCTGCGGCAACGATGCGCTTACTATGACCGGCTATACG | 46555 |
| Qy | 1262 | GCGACTTCGATTGCGGTGATAGACTGCAACAGTGTGTCACCCAGACAGTCGACTTCAGCC | 1321 |
| Db | 4656 | GCGACTTCGACTCGGTGATAGACTGCAATAGTGTGTACCCAGACAGTCGACTTTACGCC | 47155 |
| Qy | 1322 | TTGACCCCTTACCTTCAACATTAGACAAATCACGCTTCCCGAGATGCTGTCTCCGTCATC | 1381 |
| Db | 4716 | TTGACCCCTTACCTTCAACATTAGACAAATCACGCTTCCCGAGATGCTGTCTCCGCACTC | 47755 |
| Qy | 1382 | AAAGTCGGGGGTAGGACTGGGCAAGAGGAAGCCAGGCACTTACAGATTTGTGGCAACCGGGG | 14411 |
| Db | 4776 | AAAGTCGGGGGTAGGACTGGGCAAGAGGAAGCCAGGCACTTACAGATTTGTGGCAACCGGGG | 48355 |
| Qy | 1442 | AGCGTCCCTTCTGGCGATGTTGATCTCGTGTCTCTGCGAGTGCATAGACGCGGGTGTG | 1501 |
| Db | 4836 | AGCGCGCCCTCGGGCATGTTCGACTGTCTGTCTGTGATGCTTATAGACGAGGCTGTG | 48955 |
| Qy | 1502 | CTTGTGATAGACTTACCGCCCGCGCGAGACACAGATTAGGGCTAGAGCATATAGAACACC | 1561 |
| Db | 4896 | CTTGTGATAGACTACCGCCCGCGAGACTACAGTTAGGCTAGAGCGGTACATGAAACACC | 49555 |
| Qy | 1562 | CGGGACTTCCCGTGTGCCAAGACCATCTTGAATTTTGGAGGGGCTCTTACGGGCTCA | 1621 |
| Db | 4956 | CGGGGCTTCCCGTGTGCCAGGACCATCTTGAATTTTGGAGGGGCTCTTACAGGCTCA | 50155 |
| Qy | 1622 | CCCACTATGAGCGCCACTTCTTATCCCAAGAAAGAGTGGGAAAACTTCCCTATC | 1681 |
| Db | 5016 | CTCATATAGATGCCCACTTCTTATCCCAAGAAAGAGTGGGAAACCTTCTTATC | 50755 |
| Qy | 1682 | TGTTAGCGTACCAAGCCACGCTGTGCGCTAGAGCTCAAGCCCTTCCCGCTGTGGAGC | 1741 |
| Db | 5076 | TGTTAGCGTACCAAGCCACGCTGTGCGCTAGAGGCTCAAGCCCTTCCCGCATGTGGAGC | 51355 |
| Qy | 1742 | AGATGTGAATGCTGTGATCCGCTCTCAAGGCCACCTTCAATGGGCGAACACTTGTCTAT | 1801 |
| Db | 5136 | AGATGTGAATGTTGATTTGCTCTCAAGGCCACCTTCAATGGGCGAACACCTTGTCTAT | 51955 |
| Qy | 1802 | ATAGACTGGGCGCTGTCCAGATAGAGTCAACCTTGAAGCAACCAAGTCAACCAAGTATATCA | 1861 |
| Db | 5196 | ACAGACTGGGCGCTGTTCAGATATGAATCAACCTTGAAGCAACCAAGTCAACCAATATATCA | 52555 |
| Qy | 1862 | TGACATGTATGTGCGACTGACCTGAGAGGTGCTCACGAGTACTGTTGGTGTCTGTTGGCGCG | 1921 |
| Db | 5256 | TGACATGTATGTGCGGCGGCACTTGAAGGTGCTCACGAGCACTTGGGTGCTGTTGGCGCG | 53155 |
| Qy | 1922 | TTCTGGCGCTTTTGGCGCGCGTATTTGCCATTCACAGGCTGTGTGTCTATATGTATAGTA | 1981 |
| Db | 5316 | TCTGGCGCTTTTGGCGCGCGTATTTGCCATTCACAGGCTGTGTGTCTATATGTATGGGAGGG | 53755 |
| Qy | 1982 | TTGTCTTGTCCGGAAGCGCGCAATTCATACCCGACAGGGAAGTCTCTACCGGAGTTTCG | 2041 |
| Db | 5376 | TCTGTCTTGTCCGGAAGCGCGCAATTCATACCTGACAGGGAAGTCTCTTACCGGAAGTTTCG | 54355 |
| Qy | 2042 | ATGAAATGGAAGAGTGCT 2059 | |
| Db | 5436 | ATGAGATGGAAGAGTGCT 5453 | |

RESULT 14
AAT12710
ID AAT12710 standard; cDNA; 9401 BP.
XX

| Accession | Protein | Location/Qualifiers |
|----------------------------|---|---------------------|
| AC | AAT12710; | |
| XX | | |
| DT | 25-MAR-2003 (revised) | |
| DT | 15-MAY-1996 (first entry) | |
| XX | | |
| DE | Hepatitis C virus polypeptin. | |
| XX | | |
| KM | Non-A non-B hepatitis virus; NANBHV; HCV; antigen; detection; diagnosis; antibodies; ds. | |
| KM | | |
| XX | | |
| OS | Hepatitis C virus. | |
| XX | | |
| FT | Key | location/Qualifiers |
| FT | CDS | 342..9378 |
| XX | | /*tag= a |
| PN | EP693687-A1. | |
| PD | 24-JAN-1996. | |
| XX | | |
| PF | 03-APR-1991; 95EP-00114016. | |
| XX | | |
| PR | 04-APR-1990; 90US-00504352. | |
| XX | | |
| PA | (CHIR) CHIRON CORP. | |
| XX | | |
| PI | Houghton M, Choo Q, Kuo G; | |
| DR | WPI; 1996-117956/13. | |
| DR | P-PSDB; AAR90931. | |
| XX | | |
| PT | Combinations of synthetic Hepatitis C virus antigens - provide more effective diagnosis of Non-A, Non-B Hepatitis. | |
| XX | | |
| PS | Disclosure; Fig 1(A-Y); 53pp; English. | |
| XX | | |
| CC | The combination comprises an HCV antigen from the C domain (pref. C22 - AAR909316) and at least one HCV antigen from the NS3 (pref. C33c - AAR90932), NS4 (pref. C100 - AAR90933), S (pref. S2 - AAR90935) or NS5 (AAR90934) domain. The antigens may in the form of a fusion protein, a simple physical mixture, or the individual antigens commonly bound to a solid matrix. They are pref. prepred. by recombinant DNA techniques (primers are given in AAT12711-t12716), but can be synthesised or isolated from HCV using affinity chromatography. (Updated on 25-MAR-2003 to correct PF field.) | |
| CC | | |
| CC | | |
| XX | | |
| SQ | Sequence 9401 BP; 1883 A; 2860 C; 2673 G; 1985 T; 0 U; 0 Other; | |
| XX | | |
| Query Match | 86.7%; Score 1786; DB 2; Length 9401; | |
| Best Local Similarity | 91.7%; Pred. No. 0; | |
| Matches 1888; Conservative | 0; Mismatches 170; Indels | 0; Gaps 0; |
| OY | 2 TGGGGCCTTATCAGGCGCTATGCCCCAGACGACAAAGGGCCTTTGGGATGCTATATCAACA | 61 |
| DB | 3418 TGGGGCCCATTCACGGCGCTACGCGCCAGACGACAAAGGGCCTTCATGAGGTGATATCAACA | 3477 |
| OY | 62 GCTTGACCGGCGGGGACAAAACCAAGGTGAGGGTGAAGTTCAAGATGCTGCAACTGCTG | 121 |
| DB | 3478 GCTTAACTGGCGGGGACAAAACCAAGTGAAGGTGAAGTTCAGATTGTGCAACTGCTG | 3537 |
| OY | 122 CCCGACTTTCTTGGCAACCTGCATTTAACGGGGGTGTGGTGGACTGTCTACCATGGAACCG | 181 |
| DB | 3538 CCCAAACCTTCTCTGGCAACGTCATCAATGAGGGGTGTCTGGAAGTGTCTAACCAACGGGCGG | 3597 |
| OY | 182 GAACAAGGACCTTGGTGGTCAACCTTAAGGGTCTCTGTATTCAGATGTATACCAATGTGACCC | 241 |
| DB | 3598 GAAAGAGGACCTTCGCTCAACCCAAAGGGTCTCTGTGATTCAGATGTATACCAATGTGAACC | 3657 |
| OY | 242 AAGACTCTGTAGGCTGGGCGGCTCCCAAGGGTGGCGGCTATTAAACCAATGCACTTGGC | 301 |
| DB | 3558 AAGACTCTGTGGGCTGGGCGGCTCCGCAAGGTGAACCGCTATTGACACCTTGCACTTGGC | 3717 |
| OY | 302 GCTCTCTGGAACCTTTAACTGGTGCAGAGGACGCGGATGTCATTCCTGTGCGCCGAGCGG | 361 |

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Db      3718 GGTCTCGGAGCTTTAACTGGTCAAGAGGCAAGCGATGTCAATCCCGTGGCCGGCGGG 3777
Qy      362 GTGATGGCAGGGGCAAGCTGTCTTTGGCCCGGCTATCTTTACTTGAAGGCTCTCGG 421
Db      3778 GTGATAGCAGGGGCAAGCTGTGTGGCCCGGCTATCTTTACTTGAAGGCTCTCTCGG 3837
Qy      422 GAGGGCTCTGTGGCCCGGCAAGCATGCGTGGGCAATTTCAAGCGGGATGCA 481
Db      3838 GGGGTCCGTGTGTGGCCCGGCAAGCGGTCATTTTGAAGCGCGGTGTGCA 3897
Qy      482 CCCGTGAGTGTGCTAAGCGGTGCACTTTCATCCCGTGAAGACTTGAAGCAACATGA 541
Db      3898 CCGGTGAGTGTGCTAAGCGGTGCACTTATCCGTGGAAGAACTGAGAGCAACATGA 3957
Qy      542 GGTCCCGGTGTCTTCAGAACACTCTCCCAACAGAGTCCCGAGACTACCAATG 601
Db      3958 GGTCCCGGTGTCTTCAGAACACTCTCTTCACAGTGTGCCCCAGAGCTTTCAGGTGG 4017
Qy      602 CCACCTGATGCTCCCAAGGAGCGTGAAGAGCAAGAGTCCCGGCGGATGCGAG 661
Db      4018 CTCACCTCATGCTCCCAAGAGCGGCAAGAGCAAGAGTCCCGGCTGATATGAG 4077
Qy      662 CTCAGGCTACAGGTGTGTGTCTCAACCCCTCCGTGCTGCAACATGAGCTTGTGG 721
Db      4078 CTCAGGCTATAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4137
Qy      722 CTTAATGCTCAAGGCGGCTTGAATGATCTTCAATCAAGCTGGGGTGAAGCAATTA 781
Db      4138 CTTAATGCTCAAGGCGGCTTGAATGATGATCTTCAATCAAGCTGGGGTGAAGCAATTA 4197
Qy      782 CTACTGGCAGCGGCTATCAAGTATTCACAGGCAAGTTCCTTGGCGAGCGGGTGT 841
Db      4198 CCACTGGCAGCGGCTATCAAGTATTCACAGGCAAGTTCCTTGGCGAGCGGGTGT 4257
Qy      842 CAGGGGTGTCTTATGACATATATTTTGAAGAGTCCCAAGTGAAGCAATCA 901
Db      4258 CAGGGGTGTCTTATGACATATATTTTGAAGAGTCCCAAGTGAAGCAATCA 4317
Qy      902 TCTTGGGCTTGGCAGTGTCTTGAAGCAAGAGTCCCAAGTGAAGCAATCA 961
Db      4318 TCTTGGGCTTGGCAGTGTCTTGAAGCAAGAGTCCCAAGTGAAGCAATCA 4377
Qy      962 TGGCAGCGGCTATCCCGTCCGGGCTCGTACAGTGTGCGCATCTTAACATGAGAGTGG 1021
Db      4378 TGGCAGCGGCTATCCCGTCCGGGCTCGTACAGTGTGCGCATCTTAACATGAGAGTGG 4437
Qy      1022 CTCTGTCACTACCGGAGAGATCCCTTTTATGGCAAGGCTATTCCTTGAAGCAATTA 1081
Db      4438 CTCTGTCACTACCGGAGAGATCCCTTTTATGGCAAGGCTATTCCTTGAAGCAATTA 4497
Qy      1082 AGGGGGGAGACATCTCATCTTCTGCACTCAAGAAAGTGCAGAGCTGCGCGCA 1141
Db      4498 AGGGGGGAGACATCTCATCTTCTGCACTCAAGAAAGTGCAGAGCTGCGCGCA 4557
Qy      1142 AACTGGTGGGCTTGGGCGTCAATGCGGTGCTTCACTACCGGCGGCTTGAAGTGTGCGTCA 1201
Db      4558 AACTGGTGGGCTTGGGCGTCAATGCGGTGCTTCACTACCGGCGGCTTGAAGTGTGCGTCA 4617
Qy      1202 TCCCGACAGTGTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1261
Db      4618 TCCCGACAGTGTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4677
Qy      1262 GCGACTTGCATTCGGGTATGAGTGCACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1321
Db      4678 GCGACTTGCATTCGGGTATGAGTGCACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4737
Qy      1322 TTGAACCTTCACTTCACTTGAAGCAATGAGCTTCCCGAGAGTGTGTGTGTGTGTGTGTGTGT 1381
Db      4738 TTGAACCTTCACTTCACTTGAAGCAATGAGCTTCCCGAGAGTGTGTGTGTGTGTGTGTGTGT 4797
Qy      1382 AACGTGAGGATGAGCTGAGAGGAGAGCAAGGCACTTCAAGATTTGTGAGCCGGGG 1441

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Db      4798 AACGTGAGGATGAGCTGAGAGGAGAGCAAGGATCTAAGATTTGTGACCGGGGG 4857
Qy      1442 AGCGTCTTTCGGGATGTTTGAATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1501
Db      4858 AGCGTCTTTCGGGATGTTTGAATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4917
Qy      1502 CTGTGTATGAGCTTACGCGCGCGAGACCAAGTGTAGCTACGAGCATATGAAACACC 1561
Db      4918 CTGTGTATGAGCTACGCGCGCGAGACCAAGTGTAGCTACGAGCATATGAAACACC 4977
Qy      1562 CCGGACTTCCCGTGTGCAAGACCATCTTGAATTTTGGAGGGCGTCTTACCGGCTTCA 1621
Db      4978 CCGGACTTCCCGTGTGCAAGACCATCTTGAATTTTGGAGGGCGTCTTACCGGCTTCA 5037
Qy      1622 CCCAATGAGCGGCCACTTCTTATCCAGACAAAGAGTGGGAGAAACCTTCCCTATC 1681
Db      5038 CTCAATGAGTGCCTTCTTATCCAGACAAAGAGTGGGAGAAACCTTCCCTATC 5097
Qy      1682 TGGTAGCGTACCAAGCCAGCGGTGCGCTAGAGCTCAAGCCCTCCCGTGTGGAGCC 1741
Db      5098 TGGTAGCGTACCAAGCCAGCGGTGCGCTAGAGCTCAAGCCCTCCCGTGTGGAGCC 5157
Qy      1742 AGATGTGAGAGTGTGTATCCGTCTCAAGCCCACTTCATGAGGCAACCTTGTCTAT 1801
Db      5158 AGATGTGAGAGTGTGTATCCGTCTCAAGCCCACTTCATGAGGCAACCTTGTCTAT 5217
Qy      1802 ATGAGCTGGGCGCTGTCCAGATGAGTCAACCTTCAAGCCCACTTCATGAGTATTA 1861
Db      5218 ATGAGCTGGGCGCTGTCCAGATGAGTCAACCTTCAAGCCCACTTCATGAGTATTA 5277
Qy      1862 TGACATGTATGTGCGCTGACCTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1921
Db      5278 TGACATGTATGTGCGCTGACCTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5337
Qy      1922 TTTGCTGTGTTGGCCCGGATTTGCTTATCCACAGGCTGCTGTATGATGATGAGTA 1981
Db      5338 TTTGCTGTGTTGGCCCGGATTTGCTTATCCACAGGCTGCTGTATGATGATGAGTA 5397
Qy      1982 TTTGCTGTGTTGGCCCGGATTTGCTTATCCACAGGCTGCTGTATGATGATGAGTA 2041
Db      5398 TTTGCTGTGTTGGCCCGGATTTGCTTATCCACAGGCTGCTGTATGATGATGAGTA 5457
Qy      2042 ATGAATGAGAGAGTGT 2059
Db      5458 ATGAATGAGAGAGTGT 5475

RESULT 15
AAT99981
ID AAT99981 standard; DNA; 9401 BP.
XX
AC AAT99981;
XX
DT 25-MAR-2003 (revised)
XX
DT 16-MAR-1998 (first entry)
XX
DE HCV polyprotein coding sequence.
XX
KW PCR primer; amplify; HCV; hepatitis C virus; antigen combination; NS3;
KW C domain; S domain; NS5; HCV polyprotein; anti-HCV antibody; detection;
XX NS4; de.
XX
OS Hepatitis C virus.
XX
XX Key Location/Qualifiers
XX FT CDS 342..9377
XX FT /*tag= a
XX PN US5683864-A.
XX PD 04-NOV-1997.
XX PF 07-JUL-1992; 92US-00910760.

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XX 18-NOV-1987; 87US-00122714.
PR 30-DEC-1987; 87US-00139886.
PR 26-FEB-1988; 88US-00161072.
PR 06-MAY-1988; 88US-00191263.
PR 26-OCT-1988; 88US-00263584.
PR 14-NOV-1988; 88US-00271450.
PR 17-MAR-1989; 89US-00325338.
PR 20-APR-1989; 89US-00341334.
PR 21-APR-1989; 89US-00353896.
PR 18-MAY-1989; 89US-00355002.
PR 04-APR-1990; 90US-00504352.
XX
PA (CHIR) CHIRON CORP.
XX
PI Kuo G, Houghton M, Choo Q;
XX
DR WPI, 1997-548976/50.
DR P-PSDB; AAW34480.
XX
PT Combination of three hepatitis C virus antigens - used for detection of
XX specific antibodies to diagnose infection.
XX
XX Discloure; Col 25-46; 57pp; English.
XX
XX This sequence represents the Hepatitis C virus polypeptide coding
XX sequence. Fragments of this sequence can be amplified and used in the
XX combination of HCV antigens of the invention. The HCV antigen combination
XX comprises an antigen (Ag1) comprising the C domain (i.e. amino acids (aa)
XX 1-120 of the HCV polypeptide), or its immunologically reactive fragment
XX containing at least 8 aa. It also comprises two additional antigens from
XX two different polypeptide domains, including at least 8 aa from the NS3,
XX NS4, 5 or NS5 domains of the polypeptide, corresponding, respectively, to
XX aa 1050-1640; 1640-2000; 120-400 and 2000-3011 of the HCV polypeptide.
XX Alternatively, Ag1 contains at least 8 aa from the 1-122 or 9-177 aa
XX regions of the HCV polypeptide. These antigen combinations are used
XX diagnostically to detect anti-HCV antibodies, using any standard
XX immunoassay format. These antigen combinations have a broader range of
XX reactivity with antibodies than any antigen individually. (Updated on 25-
XX MAR-2003 to correct PR field.)
SQ Sequence 9401 BP; 1883 A; 2860 C; 2673 G; 1985 T; 0 U; 0 Other;
Query Match 86.7%; Score 1786; DB 2; Length 9401;
Best Local Similarity 91.7%; Pred. No. 0;
Matches 1888; Conservative 0; Mismatches 170; Indels 0; Gaps 0;
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DB 3418 TGGCCCTATCAGCGCCTATGCCCAGACAGAGGGGCTTTGGGATGATATACCA 3477
QY 62 GCTTACCGGCGGGAACAAACAGGTGAGGGGTGAGGTGATGATGCTGCACTGCTG 121
DB 3478 GCTTACCGGCGGGAACAAACAGGTGAGGGGTGAGGTGATGATGCTGCACTGCTG 3537
QY 122 CCCAATCTTTCTTGGCACTGCTATTAAGGGGTGCTGCTGCTGCTGCTGCTGCTGCTG 181
DB 3538 CCCAATCTTTCTTGGCACTGCTATTAAGGGGTGCTGCTGCTGCTGCTGCTGCTGCTG 3597
QY 182 GAACAAGACATTCGTCACCTTAAGGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 241
DB 3598 GAACAAGACATTCGTCACCTTAAGGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3657
QY 242 AAGACTGCTAGAGCTGAGCCGCTCCCAAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 301
DB 3658 AAGACTGCTAGAGCTGAGCCGCTCCCAAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3717
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DB 3838 GAGGCCCTCTGTGTGCCCCCGACAGACATGCCGTGAGATATTCAGAGCGCGGATGCA 3897
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Job time : 1265 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 7, 2006, 20:15:05 / Search time 8380 Seconds

(without alignments) 11506.942 Million cell updates/sec

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Perfect score: 2061
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Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

Database :

EST:*

1: gb_ests1:*

2: gb_ests2:*

3: gb_ests3:*

4: gb_hic:*

5: gb_ests4:*

6: gb_ests5:*

7: gb_ests6:*

8: gb_ests7:*

9: gb_gss81:*

10: gb_gss82:*

11: gb_gss83:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| C 2 | 465.4 | 22.6 | 824 | 10 | CZ990751 207976 TO |
| C 3 | 450.8 | 21.9 | 769 | 10 | CZ990230 207284 TO |
| C 4 | 385.8 | 18.7 | 852 | 10 | CZ990230 207384 TO |
| C 5 | 374.2 | 18.2 | 817 | 10 | CZ990242 207300 TO |
| C 6 | 261.4 | 12.7 | 980 | 10 | CZ934124 251577 TO |
| C 7 | 170.4 | 8.3 | 891 | 10 | CZ990535 207704 TO |
| C 8 | 142.4 | 6.9 | 922 | 10 | CZ990744 207968 TO |
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| C 10 | 44.8 | 2.2 | 935 | 10 | CNS006XK |
| C 11 | 44.4 | 2.2 | 834 | 3 | BI956973 |
| C 12 | 43.4 | 2.1 | 666 | 3 | BM950570 |
| C 13 | 43.4 | 2.1 | 793 | 8 | BM950570 UI-M-EH0P |
| C 14 | 43.4 | 2.1 | 860 | 8 | BM950570 UI-M-EH0P |
| C 15 | 42.8 | 2.1 | 1863 | 7 | CV068974 f2 new ch |
| C 16 | 42.6 | 2.1 | 633 | 3 | BI959933 |
| C 17 | 42.2 | 2.0 | 871 | 6 | CD437613 |
| C 18 | 41.8 | 2.0 | 564 | 2 | BE291962 |
| C 19 | 41.8 | 2.0 | 700 | 8 | BI155705 |
| C 20 | 41.8 | 2.0 | 935 | 5 | BO876256 |
| C 21 | 41.8 | 2.0 | 1020 | 5 | BY711719 |
| C 22 | 41.8 | 2.0 | 1020 | 5 | BY711719 |

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| C 23 | 41.8 | 2.0 | 1409 | 4 | AK012576 |
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| C 27 | 40.4 | 2.0 | 750 | 10 | CZ544987 |
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| C 30 | 40.2 | 2.0 | 629 | 2 | BS066349 |
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| C 32 | 40.2 | 2.0 | 544 | 7 | CO975862 |
| C 33 | 40.0 | 1.9 | 697 | 7 | CN944784 |
| C 34 | 39.8 | 1.9 | 624 | 4 | CD938118 |
| C 35 | 39.8 | 1.9 | 640 | 7 | CO967445 |
| C 36 | 39.8 | 1.9 | 896 | 2 | BS669273 |
| C 37 | 39.6 | 1.9 | 424 | 5 | BO665971 |
| C 38 | 39.6 | 1.9 | 429 | 5 | BO665888 |
| C 39 | 39.6 | 1.9 | 430 | 5 | BO665954 |
| C 40 | 39.6 | 1.9 | 468 | 8 | DN390574 |
| C 41 | 39.6 | 1.9 | 574 | 6 | CB873738 |
| C 42 | 39.6 | 1.9 | 595 | 5 | CA013559 |
| C 43 | 39.6 | 1.9 | 641 | 6 | CD861674 |
| C 44 | 39.6 | 1.9 | 751 | 6 | CF452146 |
| C 45 | 39.6 | 1.9 | 848 | 7 | CV069194 |

ALIGNMENTS

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DEFINITION 207380 Tomato MboI BAC library Lycopersicon esculentum genomic clone SL_MboI0131C03 5, genomic survey sequence.
ACCESSION CZ990300
VERSION CZ990300.1 GI:72341945
KEYWORDS GSS.
SOURCE Lycopersicon esculentum (Solanum Lycopersicum)
ORGANISM Lycopersicon esculentum
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REFERENCE 1 (bases 1 to 849)
Muller, L.A., Buel, R.M., Wang, Y., Tankale, S.D., Giovannoni, J.J., Van Eck, J. and Stack, S.
BAC end sequencing from three Solanum Lycopersicon libraries
Unpublished (2005)
Other GSSs: 207379
Contact: Lukas Mueller
Tankale Lab, Dept. of Plant Breeding
Cornell University, Ithaca, NY 14853, USA
Tel: 607-255-6557
Fax: 607-255-6683
Email: sgn-feedback@cornell.edu
Plate: 131 row: C column: 3
Seq primer: 17
Class: BAC ends
High quality sequence start: 25
High quality sequence stop: 464.
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/clone="SL_MboI0131C03"
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Best Local Similarity 86.0%; Pred. No. 2.9e-131;

| DEFINITION | 207284 Tomato Mboi BAC Library Lycopersicon esculentum genomic clone SL_Mboi0131A03 5, genomic survey sequence. |
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| ACCESSION | C2990230 |
| VERSION | C2990230.1 GI:72341875 |
| KEYWORDS | GS5. |
| SOURCE | Lycopersicon esculentum (Solanum Lycopersicum) |
| ORGANISM | Lycopersicon esculentum Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamiales; Solanales; Solanaceae; Solanum; Lycopersicon. |
| REFERENCE | 1 (bases 1 to 769) Mueller L.A., Bueler R.M., Wang Y., Tanksey S.D., Giovannoni J.J., Van Eck J. and Strack S. BAC end sequencing from three Solanum Lycopersicon libraries |
| AUTHORS | Unpublished (2005) |
| TITLE | Other GS5s: 207283 |
| JOURNAL | Contact: Lukas Mueller |
| COMMENT | Tanksey Lab, Dept. of Plant Breeding Cornell University 251 Emerson Hall, Ithaca, NY 14853, USA Tel: 607-255-6557 Fax: 607-255-6683 Email: sgn-feedback@sgn.cornell.edu Plate: 131 row: A column: 3 Seq primer: 17 Class: BAC ends High quality sequence start: 6 High quality sequence stop: 374. Location/Qualifiers |
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| Best Local Similarity | 88.8%; Pred. No. 1.2e-113; |
| Matches | 499; Conservative 0; Mismatches 62; Indels 1; Gaps 1 |
| D1 | 135 GGCAACTGCATTACGGGGTGTGGACTGTCAACATGAGCGGAAACAAGACAT 194 |
| D2 | 562 GACAACCTGAGCAACAGGATGGAGGAACGGTTACCAAGGGGACGAGAAATGACGTT 503 |
| D3 | 195 TGGCTACCTAAGGGTCTGTTATTCAG-ATGTACCACAATGTGACCAAGACTTGTA 253 |
| D4 | 502 GGAGTCACACAAGGAGCCTGTAGTCAGAAATGTACCAATGTGGACCAAGACTTATGG 443 |
| D5 | 254 GGTGGCCCGCTCCCAAGGTGGCCGCTCAATTAACAACAAGCACTGGCGGCTCTGGACC 313 |
| D6 | 442 GTGGCCCGGCTCCCAAGGGGCGCGCTCAATTAACACCTGCACTTGGGCTCTTGGACC 383 |
| D7 | 314 TTATCTGGTCAACGAGGACGCGGATGTCAATTCGTGTGGCGGACGAGGGTGAATGACAGG 373 |
| D8 | 382 TTATCTGGTCAACGAGGACGCGGATGTCAATTCGTGTGGCGGCGGAGGTGAACAGAG 323 |
| D9 | 374 GCAGCTGTCTTTCGCCCGGCTATATCTCTTACTTGAAGAGCTCTTGGAGGCGCTCTGC 433 |
| D10 | 322 GCAGCTGTCTTTCGCCCGGCTATATCTCTTACTTGAAGAGGCTCTTGGAGGCGCTCTGC 263 |
| D11 | 434 TGTGCCCCGAGGACATGCCGTAAGCATTTTCAGAGCGCGGATTAAGCAACCGTGAAGTGG 493 |
| D12 | 262 TGTGCCCCGAGGACATGCCGTAAGCATTTTAAGGGCGCGGATTAAGCAACCGTGAAGTGG 203 |
| D13 | 494 CTAAAGCGGTGACATTCATCCCGTGAAGAGGTTAGAGCAACCAATGAAGTCCCGGATGT 553 |
| D14 | 202 CTAAAGCGGTGACATTCATTCCTCCGTGAAGAGCTTAAGCAACCAATGAAGTCCCGGATGT 143 |
| D15 | 554 TCTCAGACAATCTCTTCCCAACAAGAGTCCCAAGACTTAACAATGAGCCACTTGATG 613 |

| Db | 142 | TCACGACAACTCTCTCCCAACAGAGTGGCCCAAGAGCTTCAGATGGCTACCTGATG | 83 |
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| Qy | 614 | CTCCACCGGAGCGGTAAAGACCAAGTCCCGGCGCATTAAGCAGCTCAGGGCTACA | 673 |
| Db | 82 | CTCCACCGGAGCGGTAAAGACCAAGTCCCGGCGCGTACGCGCTCAGGGCTACA | 23 |
| Qy | 674 | AGGTGCTGTGCTCAACCCCTC | 695 |
| Db | 22 | AGGTGCTGTGCTCAACCCCTC | 1 |
| RESULT 4 | | | |
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| DEFINITION | 207384 Tomato MboI BAC library Lycopersicon esculentum genomic clone SL_MboI0131C05 5, genomic survey sequence. | linear | GSS 11-AUG-2005 |
| ACCESSION | CT2990303 | | |
| VERSION | CT2990303.1 | GI:72341948 | |
| KEYWORDS | GSS. | | |
| ORGANISM | Lycopersicon esculentum (Solanum lycopersicum) | | |
| SOURCE | Lycopersicon esculentum Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamiales; Solanales; Solanaceae; Solanum; Lycopersicon. | | |
| REFERENCE | 1 (bases 1 to 852) Mueller, L.A., Bueler, R.M., Wang, Y., Tanksley, S.D., Giovannoni, J.J., Van Eck, J., and Stack, S. | | |
| AUTHORS | BAC end sequencing from three Solanum lycopersicon libraries Unpublished (2005) | | |
| TITLE | Other_GSSs: 207383 | | |
| JOURNAL | Contact: Lukas Mueller Tanksley Lab, Dept. of Plant Breeding Cornell University 251 Emerson Hall, Ithaca, NY 14853, USA | | |
| COMMENT | Tel: 607-255-6557 Fax: 607-255-6683 Email: sgn-feedback@sgn.cornell.edu Plate: 131 row: C column: 5 Seq primer: T7 Class: BAC ends High quality sequence start: 28 High quality sequence stop: 477. Location/Qualifiers 1..852 /organism="Lycopersicon esculentum" /mol_type="Genomic DNA" /cultivar="Heinz 1706" /db_xref="taxon:4081" /clone="SL_MboI0131C05" /lab_host="E. coli" /clone_lib="Tomato MboI BAC library" /note="Vector: pBelobAC11; site_1: MboI" | | |
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| Qy | 62 | GCTTACCGGCGCGGGAACAAAACAGGTGAGGGGTGAGTTCAAGTGTGCACTGCTG | 121 |
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| Qy | 122 | CCAGACTTTTCTTGGAACCTGATTAACGGGGTGTGTGATCTGTACCATGGAACG | 181 |
| Db | 239 | CCAGACTTTTCTTGGAACCTGATTAACGGGGTGTGTGATCTGTACCATGGAACG | 298 |
| Qy | 182 | GAACAAGACATTTGGCTACCTTAAGGTCTCTTTATCCAGATGTACCAAAATGTGACC | 241 |

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Db 359 AAGACCTGTTAGGCTGGCCCGCTCCCAAGGTGCGGCTCATTAACACCATGACTTGGC 418
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Qy 422 GAGGCTTGTGCTGTCGCGCAGG 446
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DEFINITION clone SL_MboI0131A11 5, genomic survey sequence.
ACCESSION CZ990242
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KEYWORDS GSS.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 817)
Mueller, L.A., Buel, R.M., Wang, Y., Tanksley, S.D., Giovannoni, J.J.,
Van Eck, J., and Stack, S.
BAC end sequencing from three Solanum lycopersicon libraries
Unpublished (2005)
Other GSSs: 207299
Contact: Lukas Mueller
Tanksley Lab, Dept. of Plant Breeding
Cornell University
251 Emerson Hall, Ithaca, NY 14853, USA
Tel: 607-255-6557
Fax: 607-255-6683
Email: sgn-feedback@sgn.cornell.edu
Place: 131 row: A column: 11
Seq primer: T7
Class: BAC ends
High quality sequence start: 5
High quality sequence stop: 420.
FEATURES
source location/Qualifiers
1..817
/organism="Lycopersicon esculentum"
/mol_type="genomic DNA"
/cultivar="Heinz 1706"
/db_xref="taxon:4081"
/clone="SL_MboI0131A11"
/lab_host="E. coli"
/clone_lib="Tomato MboI BAC Library"
/note="Vector: pBelBAC11; Site_1: MboI"

ORIGIN
Query Match 18.2%; Score 374.2; DB 10; Length 817;
Best Local Similarity 87.5%; Pred. No. 2.5e-92;
Matches 421; Conservative 0; Mismatches 58; Indels 2; Gaps 1;
Qy 2 TGGCGCCTATCAAGGCTATGCGCAGACAGAAAGGGGCTTTTGGATGATATACCA 61
Db 82 TGGCGCCTATCAAGGCTATGCGCAGACAGAAAGGGGCTTTTGGATGATATACCA 141
Qy 62 GCTTGACCGGCGGACAAACACAGGTGAGGGGTGAGGTTGATGCTGCACTGCTG 121
Db 142 GCCTGACCGGCGGACAAACACAGGTGAGGGGTGAGGTTGATGCTGCACTGCG 201

Qy 122 CCCAGACTTCTTGGCAACCTGCATTAACGGGGTGTGTGACTGTCTTACCATGAGCGG 181
Db 202 CCCAGACTTCTTGGCAACCTGTATTAACGGGGTGTGTGACTGTCTTACCATGAGCGG 261
Qy 182 GAACAAGACATGTCGCTACCTTAAGGGTCTGTATTCAGATGTACACCAATGTGACC 241
Db 262 GAACAAGACATGTCGCTACCTTAAGGGTCTGTATTCAGATGTACACCAATGTGACC 321
Qy 242 AAGACCTGTTAGGCTGGCCCGCTCCCAAGGTGCGGCTCATTAACACCATGACTTGGC 301
Db 322 AAGACCTGTTAGGCTGGCCCGCTCCCAAGGTGCGGCTCATTAACACCATGACTTGGC 381
Qy 302 GCTCTCGGACCTTTACCTGTGTACAGAGCAGCGGATGTCATTCCTGTCGCGCAGG 361
Db 382 GCTCTCGGACCTTTACCTGTGTGTACAGAGCAGCGGATGTCATTCCTGTCGCGCAGG 441
Qy 362 GTGATGACAGGAGGACGCTGCTTGGCCCGGCTATCTCTTAAAGGCTCTCGG 421
Db 442 GTGACAGACAGAGGACGACTGCTCTCCCGCTATCTCTTAAAGGCTCTCGG 501
Qy 422 GAGGCTTGTGCTGTG--GCCCCAGACATGCGGTGAGCATATTCAGAGCCGCTATG 479
Db 502 GGGGCCCTGCTAGCCCTCCCTCAGGACATCCGCTGTATATTTAGGACCTCGTCTG 561
Qy 480 C 480
Db 562 C 562

RESULT 6
CZ934124 980 bp DNA linear GSS 11-AUG-2005
LOCUS 251577 Tomato EcoRI BAC library Lycopersicon esculentum genomic
DEFINITION clone SL_EcoRI0030115 5, genomic survey sequence.
ACCESSION CZ934124
VERSION CZ934124.1 GI:72264385
KEYWORDS GSS.
SOURCE Lycopersicon esculentum (Solanum lycopersicum)
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 980)
Mueller, L.A., Buel, R.M., Wang, Y., Tanksley, S.D., Giovannoni, J.J.,
Van Eck, J., and Stack, S.
BAC end sequencing from three Solanum lycopersicon libraries
Unpublished (2005)
Other GSSs: 251576
Contact: Lukas Mueller
Tanksley Lab, Dept. of Plant Breeding
Cornell University
251 Emerson Hall, Ithaca, NY 14853, USA
Tel: 607-255-6557
Fax: 607-255-6683
Email: sgn-feedback@sgn.cornell.edu
Place: 30 row: I column: 15
Seq primer: T7
Class: BAC ends
High quality sequence start: 23
High quality sequence stop: 485.
FEATURES
source location/Qualifiers
1..980
/organism="Lycopersicon esculentum"
/mol_type="genomic DNA"
/cultivar="Heinz 1706"
/db_xref="taxon:4081"
/clone="SL_EcoRI0030115"
/lab_host="E. coli"
/clone_lib="Tomato EcoRI BAC Library"
/note="Vector: unk; Site_1: EcoRI"

ORIGIN

Query Match 12.7%; Score 261.4; DB 10; Length 980;
 Best Local Similarity 74.1%; Pred. No. 6; le-61;
 Matches 370; Conservative 0; Mismatches 126; Indels 3; Gaps 3;

QY 2 TGGCCCTATACAGGCTATATGCCAGACAGACAAAGGCGCTTTGGAGTGCATATACCA 61
 |||||
 DB 120 TTGCCCCCATCAAGCTTACTCCCAACAGACCGGGGCTTACTGTGTATCATCACTA 179
 |||||

QY 62 GCTTACCGGCGGGGCAAAAACAGGTGAGGTGATGATCGGTGCACTGCG 121
 |||||
 DB 180 GCTTACAGGCGGGGCAAAAACAGGTGAGGTGATGATCGGTGCACTGCG 239
 |||||

QY 122 CCCAGACTTTCTTGGCAACTGCAATTAAGGGGTGTGTGACTGTCACTGAGCGG 181
 |||||
 DB 240 CGCATCTCTCTGGGAGACTGTGTCAAGGGGTGTGTGACTGTCTTCCATGGCGCG 299
 |||||

QY 182 GAAACAAGACATTTGGGTGATCACTTAAGGTCTGTATTCAGATGTACACCAATGTGAGC 241
 |||||
 DB 300 GCTCAAAAGACCTTACCGGCGGCAAAAAGGCCCAATCACCCAATGTACACCAATGTAGAC 359
 |||||

QY 242 AAGACCTGTAGGCTGCGCGCGCTCCCAAGGTGCGCGCTCATTAACACCATGCACTTGG 301
 |||||
 DB 360 AAGACCTGTGCGGTGCGGAGCGCGCGCGCGGCGGTGCTGACACCATGCACTTGG 419
 |||||

QY 302 GCTCTCGGACCTTTACTGTCATGTCAGAGGACAGCGCATGTCCTGTGCGCGACGCG 361
 |||||
 DB 420 GCAAGCTCGGACCTTTACTGTCATGTCAGAGGACAGCGCATGTCCTGTGCGGTGCGCG 479
 |||||

QY 362 GTGATGGACGGGAGCGGCTGTTTGGCGG-CGGCTTATCTTACTTGAAGGCTTCTGG 420
 |||||
 DB 480 GCGACAGCATGGGGAGCTTACTATCCCGATGCCGCTCTCTACTTGAAGGACCTTCTCC 539
 |||||

QY 421 GGAGG-CCCTGCTGTGCGCGCGGAGAGATGCCGTAGGCA-TATTCAGAGCGCGGAT 478
 |||||
 DB 540 GGTGTGTCACCTGCTTGGCGCTCAAGGTATATGTTGCAATCTTCAAGGCTGCTTGA 599
 |||||

QY 479 GCACCGGTGAGTGGCTTA 497
 |||||
 DB 600 GCTCTGTGTGCTCTTA 618
 |||||

RESULT 7 891 bp DNA linear GSS 11-AUG-2005
 C2990535
 LOCUS 207704 Tomato MboI BAC Library Lycopersicon esculentum genomic
 DEFINITION clone SL_MboI0131121 5, genomic survey sequence.
 C2990535
 ACCESSION C2990535.1 GI:72342180
 VERSION GSS.
 KEYWORDS Lycopersicon esculentum (Solanum Lycopersicum)
 SOURCE Lycopersicon esculentum
 ORGANISM Lycopersicon esculentum (Solanum Lycopersicum)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 asterids; lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.
 1 (bases 1 to 891)
 REFERENCE Mueller,L.A., Bueler,R.M., Wang,Y., Tanksey,S.D., Giovannoni,J.J.,
 Van Eck,J. and Stack,S.
 TITLE BAC end sequencing from three Solanum Lycopersicon libraries
 JOURNAL Unpublished (2005)
 COMMENT Other GSSs: 207703
 Contact: Lukas Mueller
 Tanksley Lab, Dept. of Plant Breeding
 Cornell University
 251 Emerson Hall, Ithaca, NY 14853, USA
 Tel: 607-255-6557
 Fax: 607-255-6683
 Email: sgn-feedback@sgn.cornell.edu
 Plate: 131 row: I column: 21
 Seq primer: 17
 Claes: BAC ends
 High quality sequence start: 39
 High quality sequence stop: 261.
 FEATURES
 Location/Qualifiers

source 1..891
 /organism="Lycopersicon esculentum"
 /mol_type="genomic DNA"
 /cultivar="Heinz 1706"
 /db_xref="taxon:4081"
 /clone="SL_MboI0131121"
 /lab_host="E. coli"
 /clone_lib="Tomato MboI BAC Library"
 /note="Vector: pBelobAC11, Site_1: MboI"

Query Match 8.3%; Score 170.4; DB 10; Length 891;
 Best Local Similarity 87.9%; Pred. No. 1; le-35;
 Matches 197; Conservative 0; Mismatches 26; Indels 1; Gaps 1;

QY 2 TGGCCCTATACAGGCTATATGCCAGACAGACAAAGGCGCTTTGGAGTGCATATACCA 61
 |||||
 DB 99 TGGCCCATCAAGCGGTATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 158
 |||||

QY 62 GCTTACCGGCGGGGCAAAAACAGGTGAGGTGATGATCGGTGCACTGCTG 121
 |||||
 DB 159 GCTTACCGGCGGGGCAAAAACAGGTGAGGTGATGATCGGTGCACTGCTG 218
 |||||

QY 122 CCCAGACTTTCTTGGCAACTGCAATTAAGGGGTGTGTGACTGTCTTACATGAGCGG 181
 |||||
 DB 219 CCCAGACTTTCTTGGCAACTGCAATTAAGGGGTGTGTGACTGTCTTACATGAGCGG 278
 |||||

QY 182 GAAACAAGACAT-TGCGTCACTTAAGGCTCTGTATTCAGAT 224
 |||||
 DB 279 GAAACAAGATTAATCTCTATCAACCCCAAGCGTCTGTATTCAGAT 322
 |||||

RESULT 8 922 bp DNA linear GSS 11-AUG-2005
 C2990744
 LOCUS 207968 Tomato MboI BAC Library Lycopersicon esculentum genomic
 DEFINITION clone SL_MboI0131009 5, genomic survey sequence.
 C2990744
 ACCESSION C2990744.1 GI:72342389
 VERSION GSS.
 KEYWORDS Lycopersicon esculentum (Solanum Lycopersicum)
 SOURCE Lycopersicon esculentum
 ORGANISM Lycopersicon esculentum (Solanum Lycopersicum)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 asterids; lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.
 1 (bases 1 to 922)
 REFERENCE Mueller,L.A., Bueler,R.M., Wang,Y., Tanksey,S.D., Giovannoni,J.J.,
 Van Eck,J. and Stack,S.
 TITLE BAC end sequencing from three Solanum Lycopersicon libraries
 JOURNAL Unpublished (2005)
 COMMENT Other GSSs: 207967
 Contact: Lukas Mueller
 Tanksley Lab, Dept. of Plant Breeding
 Cornell University
 251 Emerson Hall, Ithaca, NY 14853, USA
 Tel: 607-255-6557
 Fax: 607-255-6683
 Email: sgn-feedback@sgn.cornell.edu
 Plate: 131 row: O column: 9
 Seq primer: 17
 Claes: BAC ends
 High quality sequence start: 48
 High quality sequence stop: 274.
 FEATURES
 source 1..922
 /organism="Lycopersicon esculentum"
 /mol_type="genomic DNA"
 /cultivar="Heinz 1706"
 /db_xref="taxon:4081"
 /clone="SL_MboI0131009"
 /lab_host="E. coli"
 /clone_lib="Tomato MboI BAC Library"
 /note="Vector: pBelobAC11, Site_1: MboI"

```

ORIGIN
Query Match      6.9%; Score 142.4; DB 10; Length 922;
Best Local Similarity 76.6%; Pred. No. 7.4e-28;
Matches 187; Conservative 0; Mismatches 56; Indels 1; Gaps 1;

QY 2 TGGGGCGTATGACGGCGCTTATGGCCAGACAGAGGGGCGCTTTGGGATGATATACCA 61
DB 107 TTGGCGCTATGACGGCGCTTATCTCCAGACAGCGGGGCGCTTACTGCTGATCATACCA 166
QY 62 GCTTACCGCGCGGAGCAAAAACAAGTGAAGGTGAGTTCAGATCTGTCACTGCTG 121
DB 167 GCTTACAGCGCGGAGCAAGAACAGGTGAGGGGAGGTTCAGGTGTTGACCGGGA 226
QY 122 CCCAAGCTTTCTTGGCACTGCTGATTAACGGGCTGTGTTGACTGTCTACATGAGCG 181
DB 227 CACAGTCTTTCTTGGCGACCTGCTCAATGAGCGTGTGTTGACTGTCTACATGAGCG 286
QY 102 GAACAAGACGATGTCACCTAAGGCTCTGTTAT-CCAGATGTACCAATGTGAC 240
DB 287 GCTCAAGACCTTACGCGCGCGGATGCGCCATCATCCAGTTGTACACAGTTATTA 346
QY 241 CAAG 244
DB 347 CCAG 350

RESULT 9
LOCUS CL252974 509 bp DNA linear GSS 28-JUN-2004
DEFINITION ZMMBB0601011r ZMMBB (HindIII) Zea mays genomic clone
ACCESSION CL252974
VERSION CL252974.1 GI:41356103
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogonae; Zea.
1 (bases 1 to 509)
Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C.,
Zohoverz,V., Fuks,G., Yu,Y., Wing,R. and Messing,J.
Sequencing of the maize genome at PGR (2003c)
Unpublished (2003)
CONTACT: Bharti,A.K.
Dr. Joachim Messing's lab
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
University
190 Frelinghuysen Road, Piscataway, NJ 08854, USA
Tel: 732 445 3801
Fax: 732 445 5735
Email: bharti@waksman.rutgers.edu
Seq primer: SP6
Class: BAC ends
High quality sequence start: 73.
Location/Qualifiers
1..509
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="ZMMBB0601011"
/lab_host="E. coli DH10B"
/clone_11b="ZMMBB (HindIII)"
/note="Vector: pCUI1; Site_1: HindIII; Site_2: HindIII"

ORIGIN
Query Match      2.3%; Score 46.8; DB 10; Length 509;
Best Local Similarity 50.4%; Pred. No. 0.24;
Matches 114; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

QY 1147 GTCGGGTTGGGCTAATGCGTGTACTACCGCGGCGCTTGATGTGTCGATCCG 1206

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DB 406 GTTCGTGTGGCGCTTGTGCGCGCTGTCAACCCCTTGTGTGTGCTACTGTATCGC 347
QY 1207 ACCAGTGTGACGTTGTGTGTGTGCAATGACGCGCTTCATGACCGGCTTACGGGAC 1266
DB 346 GCCCTTGTGCTATGCTGTGTGTGCGCATAGTGTGCGCTGTGCGGCTATCCCTCGCC 287
QY 1267 TTGCATTTGGTGATGATGACGACCGTGTGACACCGACAGACAGTGCATTCAGCCTGAC 1326
DB 286 GTTGCACCTTGTGCGCGTGTGCTGTACCGCGCGACCGCGCTTGTGCTGTGTGCTGT 227
QY 1327 CCTACCTTACCAATGAGACATCAAGCTTCCCGAGATGCTGTCT 1372
DB 226 GTCGCGTGTGCTGTGCGCGCATACCTGCGCATGCTTCACTT 181

RESULT 10
LOCUS CNS006XK 935 bp DNA linear GSS 03-JUN-1999
DEFINITION Drosophila melanogaster genome survey sequence T7 end of BAC #
BACR14N09 of RPCT-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION AL066051.1 GI:4945019
VERSION AL066051
KEYWORDS GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 935)
Genoscope.
Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 Evry cedex - FRANCE (E-mail : sequefgenoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see http://www.fruitfly.org The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osoegawa and
Aaron Mamoser in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCT-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain Y2; cn bw sp, the same strain used for the library
p1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
Location/Qualifiers
1..935
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR14N09"
/clone_11b="RPCT-98"
/note="end : T7"

ORIGIN
Query Match      2.2%; Score 44.8; DB 10; Length 935;
Best Local Similarity 30.9%; Pred. No. 1;
Matches 94; Conservative 64; Mismatches 146; Indels 0; Gaps 0;

QY 356 GACGGGTGATGACGAGGAGCAAGCTTTCGCGCGCTTATCTTACTTGAAGCT 415
DB 927 GSSGSSSSSSGCGGSSGCGGSSCGGSSCGGSSCGGSSCGGSSCGGSSCGGSSCGGSS 868
QY 416 CTTGGGAGGCGCTTGTGCTGTGCCCCGAGACATCCGTATGAGCATATTCAGAGCGCGG 475
DB 867 CGCCSCGSSSCSCGCGGSSGCGGSSCGGSSCGGSSCGGSSCGGSSCGGSSCGGSSCGG 808

```


/note="Organ: brain; Vector: pVX-Aac; Site 1: Ecor I; Site 2: Not I; The library was constructed according to Bonaldo, Lemmon and Soares, Genome Research, 6:791-806, 1996. Denatured mRNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was size selected according to mRNA size fraction, ligated with Ecor I adaptor, digested with Not I, and then cloned directionally into pVX-Aac vector. The library tag sequence located between the Not I site and the polyA tail, is CAGCCACGAC. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

ORIGIN

Query Match 2.1%; Score 43.4; DB 3; Length 666;
Best Local Similarity 53.9%; Pred. No. 2.3;
Matches 89; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

QY 687 CAACCCCTCGTCTGCAACATGGGCTTTGCTTACATGTCACAGCCCATGGAT 746
DB 624 CAAGCCACCTGTGCTGGAGCATTGGCTCTGCTGCTGCTGCTGCTGCTGCTGCT 565
QY 747 TGATCTTACATCAGACGCTGGGTGAGGACATTACTAGGACGCCATCAGTATTC 806
DB 564 GGACACAAAGGGGAGCTCTCGGTGAGGCAAGTTCACAGCAGCTGGGATGATGCC 505
QY 807 CACCTACGCAAGTTCTTCCGACGCGCGGTGTTTCAGGCGGTGC 851
DB 504 CGGCTCTGAGAGAGCTGCGACGCCGCGGTGGAGTTACGCTGAGGC 460

RESULT 13
LOCUS CX661874 793 bp mRNA linear EST 18-JAN-2005
DEFINITION V01011F01_559192 Fragaria vesca heat stressed seedlings cDNA library in pCMV-SPORT 6.1 Fragaria vesca cDNA clone V01011F01 3, mRNA sequence.

ACCESSION CX661874 GI:57896117
VERSION CX661874
KEYWORDS EST.
SOURCE Fragaria vesca
ORGANISM Fragaria vesca
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Rosales; Rosaceae; Rosoideae; Fragaria.
REFERENCE 1 (bases 1 to 793)
AUTHORS Shulaev, V. and Slovin, J.
TITLE Fragaria vesca EST database (FVdbEST): A tool for strawberry functional genomics
JOURNAL Unpublished (2004)
COMMENT Contact: Shulaev V
Shulaev's Lab

VBI Bioinformatics I, Washington Street, Virginia Bioinformatics Institute, Blacksburg, VA 24061, USA
Tel: 1-540-231-3489
Fax: 1-540-231-2606
Email: vshulaev@vbi.vt.edu
PCR Primers
FORWARD: M13 forward at 5' end
BACKWARD: M13 reverse 17mer at 3' end
Plate: 011 row: F column: 01
Seq primer: M13 reverse 17mer at 3' end
High quality sequence stop: 793.

FEATURES

1..793 location/Qualifiers
source
/organism="Fragaria vesca"
/mol_type="mRNA"
/db_xref="taxon:57918"
/clone="V01011F01"

ORIGIN

Query Match 2.1%; Score 43.4; DB 8; Length 793;
Best Local Similarity 50.7%; Pred. No. 2.4;
Matches 104; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

QY 1160 TCAATGCCGTGCTTACACCGGCTTGATGTCTCCGTATCCCGACCACTGTGACG 1219
DB 428 TCGAGCGCCGCCGAGAGACGCGCGTGATACATCAACCGCACCGCTGAGT 487
QY 1220 TTGTGCTGTGCAACTGACGCCCTCATGACGCGCTTACGCGCACTTGATTCGATGA 1279
DB 488 ACGAGACCGAAGAGCGCCCACTACGCCCACTGATGCTGCCGCCACCGCATTAAGTCA 547
QY 1280 TAGACTGCAACAGTGTGTCAACCCAGACAGTGCATTCAGCTTACCTTACCA 1339
DB 548 AGAATGATATCATCGGCGCGCGAGAGAGAGGCGCATCTCTGTGCTCGGCGCG 607.
QY 1340 TTGACACATACAGCTTCCCAAGA 1364
DB 608 ACGGCCAATGCGCGAGACCAAGA 632

RESULT 14

LOCUS CX661332 860 bp mRNA linear EST 18-JAN-2005
DEFINITION V01014A08_558094 Fragaria vesca heat stressed seedlings cDNA library in pCMV-SPORT 6.1 Fragaria vesca cDNA clone V01014A08 3, mRNA sequence.

ACCESSION CX661332 GI:57895575
VERSION CX661332
KEYWORDS EST.
SOURCE Fragaria vesca
ORGANISM Fragaria vesca
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Rosales; Rosaceae; Rosoideae; Fragaria.
REFERENCE 1 (bases 1 to 860)
AUTHORS Shulaev, V. and Slovin, J.
TITLE Fragaria vesca EST database (FVdbEST): A tool for strawberry functional genomics
JOURNAL Unpublished (2004)
COMMENT Contact: Shulaev V
Shulaev's Lab

VBI Bioinformatics I, Washington Street, Virginia Bioinformatics Institute, Blacksburg, VA 24061, USA
Tel: 1-540-231-3489
Fax: 1-540-231-2606
Email: vshulaev@vbi.vt.edu
PCR Primers
FORWARD: M13 forward at 5' end
BACKWARD: M13 reverse 17mer at 3' end

Plate: 014 row: A column: 08
Seq primer: M13 reverse 17mer at 3' end
High quality sequence stop: 860.
Location/Qualifiers

FEATURES

source

1. 860
/organism="Fragaria vesca"
/mol_type="mRNA"
/db_xref="taxon:57918"
/clone="V01014A08"
/dev_stage="seedlings"
/clone_11b="Fragaria vesca heat stressed seedlings cDNA library in PCWV-SPORT 6.1"
/note="Vector: PCWV-SPORT6.1; Site 1: NotI; Site 2: EcoRV; (Adopted from the Invitrogen product manual) Custom cDNA library PCWV-SPORT6.1 is prepared as follows: mRNA is isolated using two steps. First, total RNA is isolated from tissues or cells using the TRIzol Reagent. Second, mRNA is isolated from total RNA using oligo (dT) in a filter syringe. First-strand cDNA is synthesized using SuperScript III Reverse Transcriptase. Second-strand cDNA is synthesized using E. coli RNase H, E. coli DNA polymerase I, and E. coli DNA ligase. cDNA is blunt-ended using T4 DNA Polymerase and digested with Not I. cDNA is size-selected using column chromatography or agarose gel electrophoresis. Size-selected cDNA is directionally cloned into the Not I-EcoR V region of the vector (EcoR V site is destroyed during cloning). Ligation mixture is transformed into competent DH10b TI-Phage Resistant E. coli and the number of primary recombinants is determined"

ORIGIN

Query Match 2.1%; Score 43.4; DB 8; Length 860;
Best Local Similarity 50.7%; Pred. No. 2.5; Mismatches 101; Indels 0; Gaps 0;

Matches 104; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

QY 1160 TCAATGCGTGCTTACTACCGCGCTTGATGTCTCCATCCCGACAGTGTGAGC 1219
DB 461 TCGAGCGCGCGCGGAGAGACGCGCGGTGGATCAACATCAACCGCACCGTCGAGT 520
QY 1220 TTGTGTGTGGCAACTGACGCGCTTCATGACCGGCTTTACCGGCACTTGCATG 1279
DB 521 ACGAGACCGAGAGCGCCCACTACGCGCCCACTGACGCGCCCGCCACGCGATTACGTCA 580
QY 1280 TAGACTGCACACGATGTGACACCGACAGACGATGACGCTTGACCTTACCTTACCA 1339
DB 581 AGACATATATCCCGCGCGCGCGCCAGATGACGCGCGCATCTCTGTGCTCGGCGCG 640
QY 1340 TTGAGACATATCAGCGCTTCCCGAGA 1364
DB 641 ACGGCCCAATGCGCGAGACCAAGA 665

RESULT 15
CV068974 1863 bp mRNA linear EST 24-AUG-2004
LOCUS CV068974/C
DEFINITION f2_new_chopped.fasta.Contig672 Preamplified custom cDNA library in PCWVSPORT6.1 (ResGen, Invitrogen Inc.) Emilia huxleyi cDNA, mRNA
sequence.

ACCESSION CV068974 GI:51532138

VERSION CV068974

KEYWORDS EST.

SOURCE Emilia huxleyi

ORGANISM Emilia huxleyi

REFERENCE 1 (bases 1 to 1863)

AUTHORS Wahlund, T.W., Zhang, X. and Read, B.A.

TITLE Expressed Sequence Tag Profiles from Calcifying and Non-Calcifying

JOURNAL Micropaleontology (2004) in press

CONTACT: Betsy Read

Department of Biological Sciences

California State University San Marcos

333 S. Twin Oaks Valley Road, San Marcos, CA 92096-0001, USA

Tel: 760 750 4129
Email: bread@csusm.edu.

FEATURES

source

1. 1863
/organism="Emilia huxleyi"
/mol_type="mRNA"
/strain="1516"
/db_xref="taxon:2903"
/dev_stage="late log growth phase"
/clone_11b="Preamplified custom cDNA library in PCWVSPORT6.1 (ResGen, Invitrogen Inc.)"
/note="Emilia huxleyi grown in Artificial Seawater (Guillard's F/2 media)."

ORIGIN

Query Match 2.1%; Score 42.8; DB 7; Length 1863;
Best Local Similarity 48.4%; Pred. No. 4.5; Mismatches 119; Conservative 0; Mismatches 127; Indels 0; Gaps 0;

QY 1126 GACGAGCTGCGCGCAAACTGGTGGCGGTGCGTCATGCGCGGCTTACTACCGCGGC 1185
DB 1523 GACGCCACAGGCGCCATGACCGGACCGCTTCTCATAGCCGCTCCCTCCCATTTGCC 1464
QY 1186 CTGATGTGTCTCGTCATCCCGACAGATGATGATGTCGTGTCGTGCAACTGACCGCTTC 1245
DB 1463 GCGGCGCTTACCGGCTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTTC 1404
QY 1246 ATGACCGGCTTTACCGGCGGACTTGCATTTGATGATGATGATGATGATGATGATGAT 1305
DB 1403 AAGCCACCTTCCCGCTTT 1344
QY 1306 AAGTCGACTTACGCTTACGCTTACGCTTACGCTTACGCTTACGCTTACGCTTACGCTT 1365
DB 1343 GTGCGCGCGCTTCCCGCATGCGCATGCGCATGCGCATGCGCATGCGCATGCGCATGCG 1284
QY 1366 GCTGTC 1371
DB 1283 TCTGAC 1278

Search completed: February 7, 2006, 22:42:58
Job time : 8384 secs

1000 (1000)

QY 241 CAAGACCTGTAGGCTGGCCGGCTCCCAAGGTCGCCGCTCATTTAACACCATGCACTTGC 300
Db 241 CAAGACCTGTAGGCTGGCCGGCTCCCAAGGTCGCCGCTCATTTAACACCATGCACTTGC 300
QY 301 GGCTCTCGGAGACCTTTACCTGTGTCAAGAGCACGCGGATGTCTCTGTGCGCGAGCG 360
Db 301 GGCTCTCGGAGACCTTTACCTGTGTCAAGAGCACGCGGATGTCTCTGTGCGCGAGCG 360
QY 361 GGTGATGCGAGGGGAGCGCTGCTTTCGCCCGGCTATCTTTACTTGAAGGCTTCG 420
Db 361 GGTGATGCGAGGGGAGCGCTGCTTTCGCCCGGCTATCTTTACTTGAAGGCTTCG 420
QY 421 GGAGGCGCTGTGTGCGCCCGAGGACATGCGGTAGGATTAATTCAGAGCGCGGTATGC 480
Db 421 GGAGGCGCTGTGTGCGCCCGAGGACATGCGGTAGGATTAATTCAGAGCGCGGTATGC 480
QY 481 ACCCGTGAAGTGGCTTAAGCGGTGAGCTTCAATCCCGTAGAGAGCTTAGAGCAACATG 540
Db 481 ACCCGTGAAGTGGCTTAAGCGGTGAGCTTCAATCCCGTAGAGAGCTTAGAGCAACATG 540
QY 541 AGGTCCCGGGTGTCTCAGACAACTTCTCCCAACAGAGTGCCTCCAGAGCTTACCAAGTG 600
Db 541 AGGTCCCGGGTGTCTCAGACAACTTCTCCCAACAGAGTGCCTCCAGAGCTTACCAAGTG 600
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Db 601 GGCCACCTGCAATGCTCCCAACCGGAGCGGTAAAGAGCAACAGATCCCGGCGCATACGA 660
QY 661 GCTCAAGGCTCAAGAGTGTGTGTCAACCCCTCCGTGTGTCAACAATGAGGCTTGTGT 720
Db 661 GCTCAAGGCTCAAGAGTGTGTGTGTCAACCCCTCCGTGTGTGTCAACAATGAGGCTTGTGT 720
QY 721 GCTTACATGTCAAGGCGCATGAGATTTGATCTTACATAGAGCTGAGGCTGAGACAT 780
Db 721 GCTTACATGTCAAGGCGCATGAGATTTGATCTTACATAGAGCTGAGGCTGAGACAT 780
QY 781 ACTTACGAGGCGCGATCAAGTATTCACCTTACCGGAGTTCCTTTCGAGCGCGGCTGT 840
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Db 1141 AAACTGTGCGGTTGGGCGTCAATGCGGGCTTACTACCGGGCTTGAATGTCCGTC 1200
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Db 1201 ATCCGACCAAGTGTGACCTTGTGCTGTGCAACTGAGCGCCCTTACGACCGGCTTTAC 1260
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Db 1861 ATGACATGATGTGCGGCTGACCTGAGAGGTCGTCAAGAGTACTGAGGCTGCTGAGCG 1920
QY 1921 GTTCTGCTGCTTTGGCGCGGTATTCCTATCCAGAGCTGTGCTGCTATGAGTAG 1980
Db 1921 GTTCTGCTGCTTTGGCGCGGTATTCCTATCCAGAGCTGTGCTGCTATGAGTAG 1980
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Db 1981 ATTGTCTTGTCCGGAAGCCCGCAATCAATCCCGAGAGGAGTCTTACCGGAGTTC 2040
QY 2041 GATGAATGGAAGAGTGTGA 2061
Db 2041 GATGAATGGAAGAGTGTGA 2061

RESULT 2
US-09-930-591-1
; Sequence 1, Application us/09930591
; Patent No. 6960559
; GENERAL INFORMATION:
; APPLICANT: Matti Salberg
; TITLE OF INVENTION: A HEPATITIS C VIRUS NON-STRUCTURAL
; FILE OF INVENTION: NS3/4A FUSION GENE
; FILE REFERENCE: TRIPEP.02BAUS
; CURRENT APPLICATION NUMBER: US/09/930,591
; CURRENT FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: 60/225,767
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/229,175
; PRIOR FILING DATE: 2000-08-29
; PRIOR APPLICATION NUMBER: 09/705,547
; PRIOR FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1

/ LENGTH: 2061
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Hepatitis C virus NS3/4A coding region
us-09-930-591-1

Query Match 100.0%; Score 2061; DB 3; Length 2061;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2061; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 AGCTTGACCGCGCGGAGCAAAAACAGGTGAGGGGTGAGTTCAATGTCATCTGT 120
QY 121 GCCCAGACTTCTTGSCAACCTGATTAACGGGGTGTGTGACCTGTACCATGAGGC 180
DB 121 GCCCAGACTTCTTGSCAACCTGATTAACGGGGTGTGTGACCTGTACCATGAGGC 180
QY 181 GGAAACAAGAGACCATTTGCGTCACTAAGGCTCTGTTATCCAGATGTAACAATGTGAC 240
DB 181 GGAAACAAGAGACCATTTGCGTCACTAAGGCTCTGTTATCCAGATGTAACAATGTGAC 240
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DB 241 CAAGACTCTGTAGGCTGCGCGCTCCCAAGGTGCCGCTCATTAACCATGCACTTGC 300
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DB 1141 AAACGTGTGCGTGGGGGTCAATGCGGTGCTTACTACCGGCGCTGATGTGCGGT 1200
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DB 1201 ATCCGACCAAGTGTGACGTTGTGTCGTGCAACTGACGCGCTTCATGACCGGCTTTAAC 1260
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DB 1921 GTTCTGCTGCTTTGGCGCGGATTTGCTTATCCACAGGCTGTGTATAGTAGTAGG 1980
QY 1981 ATGTCTTGTGCGGAAACCGGCAATCATACCGACAGGAAAGTCTTACCGGAGTTTC 2040
DB 1981 ATGTCTTGTGCGGAAACCGGCAATCATACCGGACAGGAAAGTCTTACCGGAGTTTC 2040
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QY 2041 GATGAATGAGAGTGTCTGA 2061
Db 2041 GATGAATGAGAGTGTCTGA 2061

RESULT 3
US-08-444-818-74

/ Sequence 74, Application US/08444818
/ Patent No. 6150087
/ GENERAL INFORMATION:
/ APPLICANT: Chien, David Y.
/ APPLICANT: Rutter, William J.
/ TITLE OF INVENTION: NANBV Diagnostics and Vaccines
/ NUMBER OF SEQUENCES: 777
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Chiron Corporation
/ STREET: 4560 Horton Street
/ CITY: Emeryville
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94608-2916
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/444,818
/ FILING DATE:
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/403,590
/ FILING DATE: 14-MAR-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Harbin, Alisa A.
/ REGISTRATION NUMBER: 33,895
/ REFERENCE/DOCKET NUMBER: 0110.002
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (508)359-3876
/ TELEFAX: (508)359-3885
/ INFORMATION FOR SEQ ID NO: 74:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 7310 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 3..7310
/ US-08-444-818-74

Query Match 86.7%; Score 1786; DB 3; Length 7310;
Best Local Similarity 91.7%; Pred. No. 0;
Matches 1888; Conservative 0; Mismatches 170; Indels 0; Gaps 0;

QY 2 TGGCCCTATCATCGGCTATGCGGAGAGAGGCGCTTTGGAGATGATTAACCA 61
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QY 62 GCTTACCGGCGGAGCAAAACCAAGTGAAGGTGAGTTGAGTTCGATCGATCACTGCTG 121
Db 1789 GCTTACCGGCGGAGCAAAACCAAGTGAAGGTGAGTTGAGTTCGATCGATCACTGCTG 1848
QY 122 CCCAGACTTCTTGGCAACCTGCAATTAACGGGCTGTGTGAGCTGTCTACATGAGCG 181
Db 1849 CCCAGACTTCTTGGCAACCTGCAATTAACGGGCTGTGTGAGCTGTCTACATGAGCG 1908
QY 182 GAAACAAGACCTTGGCTGCACTAAGGGTCTGTATTCAGATGTACCAATGTGAGCC 241
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Db 2029 GCTCTCGGACCTTTACCTGTGCAAGAGCAAGCCGATGTCAATTCGTGCGCGCAGCG 2088
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Db 2509 CCACTGAGAGCCGATCACTGATTCACCTTACCGGCAATTCCTTGCAGCGCGGTGT 2568
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Db 2569 CAGGGGCTGTTATGACATTAATTTGTGACAGAGTCCACTCCAGGATGCAATCCA 2628
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Db 3109 AACGTCGGGGGAGAGCTGGCAGAGAGAGAGCCAGGACTTCAAGATTGTGGACCGGGG 3168
Qy 1442 AGCGCTCTTCTGGCAGATTGTGACTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 1501
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Qy 1502 CTGTGTATGAGCTTACGCGCGCGAGACCAAGTATGAGCTTACAGCATATGACACCC 1561
Db 3229 CTGTGTATGAGCTTACGCGCGCGAGACCAAGTATGAGCTTACAGCATATGACACCC 3288
Qy 1562 CGGACCTTCCGCTGTGCTCAAGACCATCTTGAATTGGAGAGCGCTCTTACCGGCTCA 1621
Db 3289 CGGGGCTTCCGCTGTGCTCAAGACCATCTTGAATTGGAGAGCGCTCTTACCGGCTCA 3348
Qy 1622 CCCACATGACGCGCACTTCTATCCAGACCAAGAGAGTGGGAGAACTTCCCTATC 1681
Db 3349 CTCATATGATGCTCCCATCTTCTATCCAGACCAAGAGAGTGGGAGAACTTCTTAC 3408
Qy 1682 TGGTAGCTACCAAGCCAGCTGTGCTAGAGCTCAAGCCCTCCCGCTGTGGAGCC 1741
Db 3409 TGGTAGCTACCAAGCCAGCTGTGCTAGAGCTCAAGCCCTCCCGCTGTGGAGCC 3468
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Qy 1922 TTGTGCTGTCTTGGCGCGCTATGCTATCAAGCTGTCTGTCTGTCTGTCTGTCTGTCTGT 1981
Db 3649 TTGTGCTGTCTTGGCGCGCTATGCTATCAAGCTGTCTGTCTGTCTGTCTGTCTGTCTGT 3708
Qy 1982 TTGTCTGTCTGCGGAAAGCGGCAATCATCCGACAGGAGATCTCTTACCGGAGTTGG 2041
Db 3709 TTGTCTGTCTGCGGAAAGCGGCAATCATCCGACAGGAGATCTCTTACCGGAGTTGG 3768
Qy 2042 ATGAATGAGAGTGTCT 2059
Db 3769 ATGAATGAGAGTGTCT 3786

RESULT 4
US-09-388-874-1
; Sequence 1, Application US/09388874
; Patent No. 6284249
; GENERAL INFORMATION:
; APPLICANT: Veronique Barban
; TITLE OF INVENTION: VACCINE COMPOSITION FOR PREVENTING OR
; FILE REFERENCE: PMP97-03A
; CURRENT APPLICATION NUMBER: US/09/388,874
; EARLIER FILING DATE: 1999-09-02
; EARLIER APPLICATION NUMBER: PCT/FR98/00448
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 97/02,887
; EARLIER FILING DATE: 1997-03-06
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 9379
; TYPE: DNA
; ORGANISM: Virus
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FEATURE:
; NAME/KEY: CDS
; LOCATION: (320)...(9352)
US-09-388-874-1

Query Match      86.7%; Score 1786; DB 3; Length 9379;
Best Local Similarity 91.7%; Pred. No. 0;
Matches 1888; Conservative 0; Mismatches 170; Indels 0; Gaps 0;

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; Sequence 1, Application US/09916359
; Patent No. 6538123
; GENERAL INFORMATION:
; APPLICANT: Veronique Barban
; TITLE OF INVENTION: VACCINE COMPOSITION FOR PREVENTING OR
; FILE REFERENCE: TREATING C HEPATITIS
; CURRENT APPLICATION NUMBER: US/09/916,359
; PRIOR FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: 09/388,874
; PRIOR FILING DATE: 1999-09-02
; PRIOR APPLICATION NUMBER: 97/02,887
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 9379
; TYPE: DNA
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; LOCATION: (320)...(9352)
US-09-916-359-1
Query Match 86.7%; Score 1786; DB 3; Length 9379;
Best Local Similarity 91.7%; Pred. No. 0;
Matches 1888; Conservative 0; Mismatches 170; Indels 0; Gaps 0;
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US-07-910-760-9
; Sequence 9, Application US/07910760
; Patent No. 5683864
; GENERAL INFORMATION:
; APPLICANT: Houghton, Michael
; APPLICANT: Choo, Qui-Lim
; APPLICANT: Kuo, George
; TITLE OF INVENTION: Combinations of Hepatitis C virus (HCV)
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESS: Chiron Corporation
; STREET: P. O. Box 8097 (Int. Prop. R-440)
; CITY: Emeryville
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94662-8097
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/910,760
; FILING DATE: 07-JUL-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Blackburn Esq., Robert P.
; REGISTRATION NUMBER: 30,447
; REFERENCE/DOCKET NUMBER: 0101,002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2702
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9401 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
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Db 4858 AGCGCCCTCCGGCATGTTGACTGCTGCTGCTGTGAGTGTATGACGAGGCTGTG 4917
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Qy 1982 TTGTCTTGTCCGAAAGCCGCAATCATCCGACAGGAGTCTTACCGGAGTTG 2041
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RESULT 7
US-08-440-519-9
Sequence 9, Application US/08440519
Patent No. 5712087
GENERAL INFORMATION:
APPLICANT: Houghton, Michael
APPLICANT: Choo, Qui-Lim
TITLE OF INVENTION: Combinations of Hepatitis C virus (HCV)
TITLE OF INVENTION: Antigens for Use in Immunoassays for Anti-HCV Antibodies
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: P.O. Box 8097 (Int. Prop. R-440)
CITY: Emeryville
STATE: CA
COUNTRY: U.S.A.
ZIP: 94662-8097
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,519
FILING DATE: 12-MAY-1995
CLASSIFICATION: 530
PRIOR APPLICATION NUMBER: US 07/910,760
FILING DATE: 07-JUL-1992

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| OY | 362 | GTGATGGAGAGGGGAGCCTGTGCTTTGAGCCCGGCTCATCTTTACTTTGAAAGGCTCTGCG | 421 |
| Dp | 3778 | GTGATAGAGAGGGGAGCCTGTGTGCGCCCGGCTCATCTTTACTTTGAAAGGCTCTGCG | 3837 |
| OY | 422 | GAGGCGCTCTGTGTGCCCCGAGGACATGCGGTAGAGATATTCAGACCGCGGTATGCA | 481 |
| Dp | 3838 | GAGGCGCGCTGTGTGCGCCCGGGGGACGCGGTGGCATATTTAGGCGCGGGTGTGCA | 3897 |
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| OY | 962 | TGCGCACCGCTAACCCCTCGGGGCTCGTCACTGTGCCCCCATCTTAATCATGAGAGGTTG | 1021 |
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| OY | 1022 | CTGTGTCCACTACCGGAGAGATCCCGCTTTATGGCAAGGCTAATCCCTTGAAGCAATTA | 1081 |
| Dp | 4438 | CTGTGTCCACCAACCGGAGAGATCCCGCTTTATGGCAAGGCTAATCCCGCTGGAATATCA | 4497 |
| OY | 1082 | AGGGGGGAGACATTTCACTTTCTGCGCACTCAAAAGAAAGTGGCAGAGCTCGCGGCA | 1141 |
| Dp | 4498 | AGGGGGGAGACATTTCACTTTCTGCTCATTAAMAAAGTGGCAGACCAATCGCGCGCA | 4557 |
| OY | 1142 | AACTGTGTGCGTTGGGCGTCAATGCGTGGCTTATACCGCGGCTTATATGTGTCCGTCA | 1201 |
| Dp | 4558 | AGCTGTGTGATTTGGGCAATCAATGCGGTGGCTTATACCGCGGCTTATATGTGTCCGTCA | 4617 |
| OY | 1202 | TCCGACCAAGTGTGACGTTGTGCTGTGTGGCAACTGACGCCCTCATGACCGGCTTTACG | 1261 |

[illegible]

STREET: P.O. Box 8097 (Int. Prop. R-440)
CITY: Emeryville
STATE: CA
COUNTRY: U.S.A.
ZIP: 94662-8097
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,549
FILING DATE: 12-MAY-1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/910,760
FILING DATE: 07-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Blackburn Esq., Robert P.
REGISTRATION NUMBER: 30,447
REFERENCE/DOCKET NUMBER: 0101.002
TELEPHONE: (510) 601-2702
TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 9401 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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OTHER INFORMATION: /note="This amino acid position
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; OTHER INFORMATION: can also be Pro."
US-08-440-549-9

Query Match 86.7%; Score 1786; DB 3; Length 9401;

Best Local Similarity 91.7%; Pred. No. 0;
Matches 1888; Conservative 0; Mismatches 170; Indels 0; Gaps 0;

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DB 3418 TGGCCGCTTACAGCGCTTATGCCAGACAGACAAAGGGGCTTTTGGATATGATATACCA 3477
QY 62 GCTTGACGGCGGGGACAAAAACAGAGTGAAGGTGAGTTGAGATGATGATCACTGCTG 121
DB 3478 GCTTGACGGCGGGGACAAAAACAGAGTGAAGGTGAGTTGAGATGATGATCACTGCTG 3537
QY 122 CCACAGCTTCTTGAGCACTGATTTACGGGGTGTGTGACTGTCTACATGAGACCG 181
DB 3538 CCACAGCTTCTTGAGCACTGATTTACGGGGTGTGTGACTGTCTACATGAGACCG 3597
QY 182 GAACAAAGACATTTGGTGTCACTTAAGGGTCTGTATCCAGATGTACCAATGTGAGAC 241
DB 3598 GAACAAAGACATTTGGTGTCACTTAAGGGTCTGTATCCAGATGTATACCAATGTAGAC 3657
QY 242 AAGACCTGTAGGGCTGGCCGGCTCCCAAGTGGCCGGCTCATTTAACCATGCACTTGG 301
DB 3658 AAGACCTGTAGGGCTGGCCGGCTCCCAAGTGGCCGGCTCATTTAACCATGCACTTGG 3717
QY 302 GCTCTCGACCTTTACCTGTGTACAGAGCAAGCCAGATGATCTCTGTGCGCCGACGG 361
DB 3718 GCTCTCGACCTTTACCTGTGTGTACAGAGCAAGCCAGATGATCTCTGTGCGCCGACGG 3777
QY 362 GTGATGACAGGGGACAGCTGTCTTGGCCCGCTTATCTTTACTTGAAGGTCTCTCG 421
DB 3778 GTGATGACAGGGGACAGCTGTCTTGGCCCGCTTATCTTTACTTGAAGGTCTCTCG 3837
QY 422 GAGGCGCTGTGCTGTGCGCCGACAGATGCGGTAGGCAATTCAGAGCGGGTATGCA 481
DB 3838 GAGGCGCTGTGCTGTGCGCCGACAGATGCGGTAGGCAATTCAGAGCGGGTATGCA 3897
QY 482 CCGGTGAGTGTGCTTAAGGGCGGTGATCTTATCCCGGTAGAGCTTGAAGCAACCATGA 541
DB 3898 CCGGTGAGTGTGCTTAAGGGCGGTGATCTTATCCCGGTAGAGCACTTGAAGCAACCATGA 3957
QY 542 GGTCTCCGGGTGTCTGACAACTCTCTCCACAGAGTGGCCAGAGCTTACCAAGTGG 601
DB 3958 GGTCTCCGGGTGTCTGACAACTCTCTCTCCACAGAGTGGCCAGAGCTTACCAAGTGG 4017
QY 602 CCGACCTGATGCTCCACCGGAGGGGTGAAGGACCAAGGTCGGGCGGATACGACG 661
DB 4018 CCGACCTGATGCTCCACCGGAGGGGTGAAGGACCAAGGTCGGGCGGATATGACG 4077
QY 662 CTCAAGGGCTTAAGAGTGTGTGCTCAACCCCTCGTTGCTGCAACATGAGGCTTGTG 721
DB 4078 CTCAAGGGCTTAAGAGTGTGTGCTCAACCCCTCGTTGCTGCAACATGAGGCTTGTG 4137
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DB 4138 CTTAACATGTCAGAGGCCATGGGATGTATCTTAACATCAAGAGCTGGGGTGAAGCAATTA 4197
QY 782 CTACAGGGAGCCGACATGATTTCCACTTAAGGCAAGTTCCTTGGCCGAGCGGGGTGT 841
DB 4198 CTACAGGGAGCCGACATGATTTCCACTTAAGGCAAGTTCCTTGGCCGAGCGGGGTGT 4257
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DB 4258 CAGGGGGTCTTATGACATTAATTTGTAAGAGTGCATCTCAAGATGCAATTCAC 4317
QY 902 TCTTGGGCAATTGGCACTGTCTTGAACCAAGAGAGCCGGGGGGGAGACATGACTGTGC 961
DB 4318 TCTTGGGCAATTGGCACTGTCTTGAACCAAGAGAGCTGGGGGGGAGACATGACTGTGC 4377

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QY 1022 CTCTGTCCACTACCGGAGAGATCCCTTTTATGCGAAGGCTATTTCCCTTGAAGCAATTA 1081
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QY 1082 AGGGGGGGGAGATCTTCTTGTGCACTCAAGAGAGAGTGCAGAGCTGCGCGCAA 1141
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QY 1322 TTGACCTTACCTTCAACATGAGACATCAAGCTTCCCGAGATGCTGTCTCCGATCTC 1381
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QY 1442 AGCGTCTTCTGCGCAATGTTGACTGTGTCTCTGCGGAGTGTATGACGGGGGTGTG 1501
DB 4858 AGCGTCTTCTGCGCAATGTTGACTGTGTCTCTGCGGAGTGTATGACGGGGGTGTG 4917
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DB 4918 CTTGTATGAGCTTACGCGCGCGAGACACAGTTAGGCTTACAGCATATGACACCC 4977
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QY 1622 CCGACATGAGCGCCCATCTTCCATCCAGACCAAGAGAGTGGGGAAACCTTCCCTATC 1681
DB 5038 CCGACATGAGCGCCCATCTTCCATCCAGACCAAGAGAGTGGGGAAACCTTCCCTATC 5097
QY 1682 TGGTAGCGTACCAAGCACCGGTGCGCTAGAGCTCAAGCGCCCTCCCGTGTGGAGAC 1741
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QY 1802 ATAGACTGGGCGCTGTCCGAATGAAAGTCAACCTTACCGACCCAGTCAACCAATATACA 1861
DB 5218 ATAGACTGGGCGCTGTGAAATGAAATCAACCTTACCGACCCAGTCAACCAATATACA 5277
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DB 5278 TGACATGTATGTGCGGCGACCTGAGAGTGTGACAGAGCTGAGGCTGCTGTGGCGGCG 5337
QY 1922 TTCTGGCTGCTTTGGCGCGGATTTGCTTATCAAGGCTGCGTGTATATGATGATGAGA 1981
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DB 5398 TTGTCTTGTCCGGAAGCCGGGAATCATACCGGAGAGTCTCTTACCGAGAGTTGG 5457
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RESULT 9

US-08-823-895A-25
Sequence 25, Application US/08823895A

Patent No. 6433159

GENERAL INFORMATION:

APPLICANT: Kevin P. Anderson

TITLE OF INVENTION: Compositions And Methods For

TITLE OF INVENTION: Treatment Of Hepatitis C Virus-Associated Diseases

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:

ADDRESSEE: Jane Massey Licata, Esq.

STREET: 66 E. Main Street

CITY: Marlton

STATE: NJ

COUNTRY: USA

ZIP: 08053

COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE

COMPUTER: IBM 486

OPERATING SYSTEM: WINDOWS FOR WORKGROUPS

SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/823,895A

FILING DATE: March 17, 1997

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/453,085

FILING DATE: May 30, 1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/945,289

FILING DATE: September 10, 1992

ATTORNEY/AGENT INFORMATION:

NAME: Jane Massey Licata

REGISTRATION NUMBER: 32,257

REFERENCE/DOCKET NUMBER: ISPH-0203

TELECOMMUNICATION INFORMATION:

TELEPHONE: (609) 779-2400

TELEFAX: (609) 810-1454

INFORMATION FOR SEQ ID NO: 25:

SEQUENCE CHARACTERISTICS:

LENGTH: 9401

TYPE: Nucleic

STRANDEDNESS: Single

TOPOLOGY: Linear

ANTI-SENSE: NO

US-08-823-895A-25

Query Match 86.7%; Score 1786; DB 3; Length 9401;

Best Local Similarity 91.7%; Pred. No. 0;

Matches 1888; Conservative 0; Mismatches 170; Indels 0; Gaps 0;

Db 2 TGGCGGCTATACGGGCTATGCGGACGAGACAAAGGGGCGCTTTGGGATGATTAATACCA 61

Db 3418 TGGCGGCTATACGGGCTATGCGGACGAGACAAAGGGGCGCTTGGGATGATTAATACCA 3477

Db 62 GCTTGACCGGCGGAGCAAAAACAGGTGAGGAGGTTGAGTCTGTCAACTGCTG 121

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Db 3538 CCGAAACCTTCTGTGGCAAGGTGATCAATGGGGTGTGTGGACTGTCTACATGAGCCG 3597

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Db 4318 TCTTGGGATTTGGCACTGTCTTGAACAAGACAGACGCGGGGCGAGACTGATGTGC 4377

Db 962 TCGCCACGCTACCCCTCGGGCTCGGTCACTGTGCCCATCTTAACATGAGAGTGG 1021

Db 4378 TCGCCACGCTACCCCTCGGGCTCGGTCACTGTGCCCATCTTAACATGAGAGTGG 4437

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Db 4438 CTCTGTCCATTAACCGGAGATCCCTTTTATGCAAGGCTTATCCCTTGAAGCAATTA 4497

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DB 5458 ATGAATGGAAGTGTCT 5475

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/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US91/02225
/ FILING DATE: 19910329
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: CIOTTI, THOMAS E.
/ REGISTRATION NUMBER: 21, 013
/ REFERENCE/DOCKET NUMBER: 2300-0101.44
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 327-7250
/ TELEFAX: (415) 327-2951
/ TELEX: 706141
/ INFORMATION FOR SEQ ID NO: 9:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 9401 base pairs
/ TYPE: NUCLEIC ACID
/ STRANDEDNESS: unknown
/ TOPOLOGY: unknown
/ MOLECULE TYPE: DNA (genomic)
/ PCT-US91-02225-9

Query Match 86.6%; Score 1785.2; DB 6; Length 9401;
Best Local Similarity 91.5%; Pred. No. 0;
Matches 1883; Conservative 6; Mismatches 169; Indels 0; Gaps 0;

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QY 362 GTGATGAGAGGAGGAGCGCTGCTTGGCGCGCGCTATCTTAACTTGAAGGCTCTGCG 421
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DB 4018 CCACCTGATGCTCCACCGGAGCGGTAAAGAGCAAGGTCCCGGCGGATATGAG 4077
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DB 4078 CTGAGGCTTATAGAGTGTGCTCAACCTCTCGTTGCTGCAACATGAGGCTTGTG 4137

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/ RESULT 10
/ PCT-US91-02225-9
/ Sequence 9, Application PC/TUS9102225
/ GENERAL INFORMATION:
/ APPLICANT: HOUGHTON, MICHAEL
/ APPLICANT: CHOO, QUI-LIM
/ APPLICANT: KUD, GEORGE
/ TITLE OF INVENTION: COMBINATIONS OF HEPATITIS C VIRUS
/ TITLE OF INVENTION: ANTIBODIES
/ NUMBER OF SEQUENCES: 10
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Morrison & Foerster
/ STREET: 545 Middlefield Road, Suite 200
/ CITY: Menlo Park
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94025
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25

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Db 1204 TGGCCGCCATCAAGGCGTACGCCCAAGACAAAGGGGCTCTTAAGGGTGCATATACCA 1263
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Db 1324 CCCAAACCTTCTGGGCACTGCAATTAAGGGGTGTGGAAGTGTCTGCACTGAGCCG 1383
Qy 182 GAACAAGACCAATGGGTGCACTTAAGGGTCTGTATTCAGATGTACACCAATGTGACC 241
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Qy 242 AAGACTGTGAGTGGGCGGGGCTCCCAAGGTGCGGCTCATTTACACCATGCACTTGG 301
Db 1444 AAGACTGTGAGTGGGCGGGGCTCCCAAGGTGCGGCTCATTTACACCATGCACTTGG 1503
Qy 302 GCTCCCTGGACCTTTAAGCTGTGCAAGGACAGCCGATGTCATTCCTGTGCGCGACGG 361
Db 1504 GCTCCCTGGACCTTTAAGCTGTGCAAGGACAGCCGATGTCATTCCTGTGCGCGACGG 1563
Qy 362 GTGATGGCAAGGGGCAAGCTGTTCGCCCCGCTATCTTTAAGTGAAGGCTCCTCG 421
Db 1564 GTGATGGCAAGGGGCAAGCTGTTCGCCCCGCTATCTTTAAGTGAAGGCTCCTCG 1623
Qy 422 GAGGCCCTTGTCTGTGCGCCGCAAGCATGCGGTAGGCATTTACAGAGCGCGGTATGCA 481
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Db 3244 ATGAATGAGAGAGTGTCT 3261

RESULT 12
US-08-444-818-88
; Sequence 88, Application US/08444818
; Patent No. 6150087
; GENERAL INFORMATION:
; APPLICANT: Chien, David Y.
; APPLICANT: Ruteer, William J.

TITLE OF INVENTION: NANBV Diagnostics and Vaccines
NUMBER OF SEQUENCES: 777
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,818
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/403,590
FILING DATE: 14-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Harbin, Alisa A.
REGISTRATION NUMBER: 33,895
REFERENCE/DOCKET NUMBER: 0110.002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508)359-3876
TELEFAX: (508)359-3885
INFORMATION FOR SEQ ID NO: 88:
SEQUENCE CHARACTERISTICS:
LENGTH: 8316 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..8316
US-08-444-818-88

Query Match 86.6%; Score 1784.4; DB 3; Length 8316;
Best Local Similarity 91.7%; Pred. No. 0;
Matches 1887; Conservative 0; Mismatches 171; Indels 0; Gaps 0;

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QY 542 GGTCCCGGTGTTCAGACAATCTCTCCCAAGCAGAGTGGCCGAGCTACCAAGTGG 601
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DB 4655 TCCTGGCTGCTTGGCGCGGATTTGCTTATCAACAGGCTGCTGCTATAGTAGTAGGA 4714
QY 1982 TTGCTGTGCGGAAAGCCGGAATCATATCCCGACAGGGAAGTCTCTTACCGGAGTTCC 2041
DB 4715 TCGTCTTGTCCGGAAAGCCGGAATCATATCCCGACAGGGAAGTCTCTTACCGAGTTCC 4774
QY 2042 ATGAATGAGAGAGTCT 2059
DB 4775 ATGAGATGAGAGAGTCT 4792

RESULT 13
US-08-444-818-137
; Sequence 137, Application US/08444818
; Patent No. 6150087
; GENERAL INFORMATION:
; APPLICANT: Chien, David Y.
; APPLICANT: Rutter, William J.
; TITLE OF INVENTION: NANBV Diagnostics and Vaccines
; NUMBER OF SEQUENCES: 777
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,818
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,590
; FILING DATE: 14-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Harbin, Alisa A.
; REGISTRATION NUMBER: 33,895
; REFERENCE/DOCKET NUMBER: 0110.002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508)359-3876

TELEFAX: (508)359-3885
; INFORMATION FOR SEQ ID NO: 137:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8987 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..8985
; US-08-444-818-137

Query Match 86.6%; Score 1784.4; DB 3; Length 8987;
Best Local Similarity 91.7%; Pred. No. 0;
Matches 1887; Conservative 0; Mismatches 171; Indels 0; Gaps 0;

QY 2 TGGCGCTTATGACGCGCTATGCGCCAGACAGAGGCGCTTTGGAGTGAATATCACCA 61
DB 3077 TGGCGCCATCAGCGCGTACCGCCAGACAGAGGCGCTCTAGGTGATATACCA 3136
QY 62 GCTTGAACCGCGCGGACAAAAACAGGTGAGGTTGAGGTTCAATGCTGCTG 121
DB 3137 GCTTAACTGCGCGGACAAAAACAGGTGAGGTTGAGGTTCAATGCTGCTG 3196
QY 122 CCCAGACTTTGCGCAACCTGCAATTAACGGGAGTGTGACGTGCTTACCATGAGCGC 181
DB 3197 CCCAACTCTCTGCAACGTGATATGAGGAGTGTGAGCTTCTTACCAACGGGCGC 3256
QY 182 GAACAGAGACCATTCGCTACCTTAAGGCTCTTATCAGATGACCAATGTGACC 241
DB 3257 GAACAGAGACCATTCGCTACCTTAAGGCTCTTATCAGATGACCAATGTGACC 3316
QY 242 AAGACTGTGAGCTGCGCGCTCCCAAGGTGCGCGCTCATTAACCATGACTTGGC 301
DB 3317 AAGACTGTGAGCTGCGCGCTCCCAAGGTGCGCGCTCATTAACCATGACTTGGC 3376
QY 302 GCTCCTGGAGCCTTAACTTGAAGTCAAGAGGACGCGAGTGTATCTGTGCGACGAG 361
DB 3377 GCTCCTGGAGCCTTAACTTGAAGTCAAGAGGACGCGAGTGTATCTGTGCGAG 3436
QY 362 GTGATGAGAGGAGGACGCTGCTTTGCGCGCGCTATCTTAAAGGCTCTCGG 421
DB 3437 GTGATGAGAGGAGGACGCTGCTTTGCGCGCGCTATCTTAAAGGCTCTCGG 3496
QY 422 GAGCCCTCTGCTGTGCGCGCGAGACATGCCGTGAGCATTTAGAGCCGCGGTATGCA 481
DB 3497 GAGCCCTCTGCTGTGCGCGCGAGACATGCCGTGAGCATTTAGAGCCGCGGTATGCA 3556
QY 482 CCCGTGAGTGGCTAAGCGGAGGCTTATCTATCCCGTGAAGAGCTTAGAGCAACATGA 541
DB 3557 CCCGTGAGTGGCTAAGCGGAGGCTTATCTATCCCGTGAAGAGCTTAGAGCAACATGA 3616
QY 542 GGTCCCGGTGTTCTCAGACAACTCTCCACAGAGTGGCCCGACGACTCAAGTGG 601
DB 3617 GGTCCCGGTGTTCTCAGACAACTCTCTCCACAGAGTGGCCCGACGACTCAAGTGG 3676
QY 602 CCCACTGATGCTCCACCGGACGCGTAAAGACACCAAGTCCCGCGCATACGAG 661
DB 3677 CTCACCTCAGTCTCCACAGGACGCGCAAAAGACCAAGTCCCGCGCATATGACG 3736
QY 662 CTCAGGGCTAAGAGTGTGAGTCAACCCCTCGGTGCTGACATAGGCTTTGGG 721
DB 3737 CTCAGGGCTAAGAGTGTGAGTCAACCCCTCGGTGCTGACATAGGCTTTGGG 3796
QY 722 CTTATATGTCAGAGCCCATGGATGATTCCTTAACATGAGACTGGGTGAGACATTA 781
DB 3797 CTTATATGTCAGAGCCCATGGATGATTCCTTAACATGAGACTGGGTGAGACATTA 3856
QY 782 CTACTGAGAGCCCATGATCACTTACCTTACCTTACCTTACCTTACCTTACCTTACCT 841
DB 3857 CCACGTGAGAGCCCATGATCACTTACCTTACCTTACCTTACCTTACCTTACCTTACCT 3916

| | | | |
|----|------|---|------|
| OY | 842 | CAGGGGGGTGCTTATATGACATTAATATTTGTAGAGAGTGGCACTCCACGGATGACATCTCA | 901 |
| Db | 3917 | CGGGGGGGCGCTTATATGACATTAATATTTGTAGAGAGTGGCACTCCACGGATGACATCTCA | 3976 |
| OY | 902 | TCCTTGGGCGATTGGACATGCTGCTCTTGACCAAGCAGAGACCGGGGGGCGAGACTGACCTGTC | 961 |
| Db | 3977 | TCCTTGGGCGATTGGACATGCTGCTCTTGACCAAGCAGAGACTGCGGGGGCGAGACTGCTTGTGC | 4036 |
| OY | 962 | TGCGCACGCTACCCCTCGGGGCTCGGTCACTGTGCCCCATCTTAACATCGAGAGGTTG | 1021 |
| Db | 4037 | TCGCGCACGCGCACCCCTCGGGGCTCGGTCACTGTGCCCCATCTTAACATCGAGAGGTTG | 4096 |
| OY | 1022 | CTCTGTCCACTTCACCGGAGAGATTCCTCTTTATGTGGAAGGCTATTCCCTTGAAGCATTA | 1081 |
| Db | 4097 | CTCTGTCCACTTCACCGGAGAGATTCCTCTTTATGTGGAAGGCTATTCCCTTGAAGCATTA | 4156 |
| OY | 1082 | AGGGGGGGGAGACATCTCATCTTTCTGCGCACTCAAAAGAGGCGAGAGGCTCGCGGAA | 1144 |
| Db | 4157 | AGGGGGGGGAGACATCTCATCTTTCTGCGCACTCAAAAGAGGCGAGAGGCTCGCGGAA | 4216 |
| OY | 1142 | AACTGTCGCGTTTGGGCGTCAATGCGTGGCTTTACTACCGGGCTTGATGTGCTGTCA | 1201 |
| Db | 4217 | AGCTGTGGCAATTGGGCGATCAATGCGGTGGCTTACTACCGGGCTTGTACGTGTCCGTCA | 4276 |
| OY | 1202 | TCCGCACCAATGTGTGACGTTGTGCTGTGGCACTGACGCGCTCATGACCGGCTTTACG | 1261 |
| Db | 4277 | TCCGCACCAAGGGCGCATGTGTGCTGTGGCAACGAGTCCCTCAATGACCGGCTTTACG | 4336 |
| OY | 1262 | GCGACTTGGATTCCGGGTATGACTGCGACAAGTGGTGACCGCGACGCACTGCACTTCAACC | 1321 |
| Db | 4337 | GCGACTTGGACTCGGTGTGATGACTGCGAATGCTGTGTGACCCGACAGAGTGCATTTCAACC | 4396 |
| OY | 1322 | TTGACCTTACCTTTCACCAATTGAGACAATACGCTTCCCGAGGATCTGTCTCCGCTATC | 1381 |
| Db | 4397 | TTGACCTTACCTTTCACCAATTGAGACAATACGCTTCCCGAGGATCTGTCTCCGCTATC | 4456 |
| OY | 1382 | AAAGCTCGGGGTATGAGACTGGCGAGAGGGAAGCAGAGCATCTACAGATTTGTGGCACCGGGG | 1441 |
| Db | 4457 | AAAGCTCGGGGCGAGACTGGCGAGGGGGAAGCAGAGCATCAACAGATTTGTGGCACCGGGG | 4516 |
| OY | 1442 | AGCGCTCTTGGGCGATGTTTGAATCTGCTGCTCTGAGAGGTGCTATAGACCGGGTTGTG | 1501 |
| Db | 4517 | AGCGCGCTCTCGGCAATGTTTGAATCTGCTGCTCTGAGAGGTGCTATAGACCGAGCTGTG | 4576 |
| OY | 1502 | CTTGGTATGAGCTTTCAGCGCCGCGAGACCAAGTTAGGCTACGAGCATATGAAACACC | 1561 |
| Db | 4577 | CTTGGTATGAGCTTCAGCGCCGCGAGACTACAGTTAGGCTACGAGCATATGAAACACC | 4636 |
| OY | 1562 | CGGAGCTTCCGCTGTGCCAAGACATCTTGAATTTTGGAGGGCGCTTTTACGGGCTTCA | 1621 |
| Db | 4637 | CGGGGCTTCCGCTGTGCCAAGACATCTTGAATTTTGGAGGGCGCTTTTACAGGGCTTCA | 4696 |
| OY | 1622 | CCCAATATGACGCCCATCTTCCATATCCGACGAACAAGCAGAGTGGGAAAACTTCCCTATC | 1681 |
| Db | 4697 | CTCATATATGATGCCCATCTTCTATCCAGACAAACAGAGTGGGAGAACTTCTTTCACC | 4756 |
| OY | 1682 | TGGTATGCGTACCAACCGAGTGTGCGCTAGAGCTCAAGACCCCTCCCGTGTGGAGCC | 1741 |
| Db | 4757 | TGGTATGCGTACCAAGCCAGCTGTGTGCGCTTAGGGCTCAAGACCCCTCCCGATGTGGAGCC | 4816 |
| OY | 1742 | AGATGTGGAAGTGTGATTCGCTCTCAAGCCCAACCTTCATGTGGGCAACACTCTGTCTAT | 1801 |
| Db | 4817 | AGATGTGGAAGTGTGATTCGCTCTCAAGCCCAACCTTCATGTGGGCAACACTCTGTCTAT | 4876 |
| OY | 1802 | ATAGACTGGGCGCTGTCCAGATGAAATGACCTCTGACGCACCCAATCAACAGTACCAATATATCA | 1861 |
| Db | 4877 | ACAGACTGGGCGCTTGTTCAGATGAAATCACCTCTGACGCACCCAATCAACAAATATCAATCA | 4936 |
| OY | 1862 | TGACATGTATGTCCGCTGACCTGGAGGTGCTGACAGATACCTGGGTGCTGTTGGCGGCG | 1921 |
| Db | 4937 | TGACATGTATGTCCGCGACCTGGAGGTGCTGACAGACCTGGGTGTCTGTTGGCGGCG | 4996 |
| OY | 1922 | TTCTGCGTGTGTCGCGGTATTCCTCATCCACAGGCTGCGTGTCTATAGTAGTAGTA | 1981 |

| DB | Accession | Sequence | Score | Length | DB | Accession | Sequence | Score | Length | DB | Accession | Sequence | Score | Length | DB | Accession | Sequence | Score | Length | | | | | |
|---|-----------|--|-------|--------|----|-----------|---|-------|--------|----|-----------|---|-------|--------|----|-----------|---|-------|--------|----|------|---|-------|------|
| Db | 4997 | TCCTGGCTGCTTTGGCCGCGGATTCCTGTAACAGAGCTGCTGATCAATGAGGCGACGG | 91.7% | 9185 | Db | 182 | GACACAGACCATTCGCTCACTTAAGGGTCTCTGTATTCAGATGTACCAATGTGAC | 86.6% | 9185 | Db | 3516 | CCCAAACTTCTTGACCAAGTGCATCAATGAGGGTGTCTGACCTGTCAACCGGGGCTG | 85.7% | 9185 | Db | 3516 | CCCAAACTTCTTGACCAAGTGCATCAATGAGGGTGTCTGACCTGTCAACCGGGGCTG | 85.7% | 9185 | Db | 3516 | CCCAAACTTCTTGACCAAGTGCATCAATGAGGGTGTCTGACCTGTCAACCGGGGCTG | 85.7% | 9185 |
| Qy | 1992 | TTGCTTTTCGGAAGCGCGCAATTCATACCCGACAGGAGTCTTACCGGAGTTG | 91.7% | 9185 | Qy | 122 | CCGAGACTTTTGTGGCAACCTGCAATTAACGAGGCTGTGTGACCTGTCAACATGGAGCG | 86.6% | 9185 | Qy | 122 | CCGAGACTTTTGTGGCAACCTGCAATTAACGAGGCTGTGTGACCTGTCAACATGGAGCG | 86.6% | 9185 | Qy | 122 | CCGAGACTTTTGTGGCAACCTGCAATTAACGAGGCTGTGTGACCTGTCAACATGGAGCG | 86.6% | 9185 | Qy | 122 | CCGAGACTTTTGTGGCAACCTGCAATTAACGAGGCTGTGTGACCTGTCAACATGGAGCG | 86.6% | 9185 |
| Db | 5057 | TCGCTTTTCCGGGAAGCGCGCATTCATCCTGACAGGAGTCTCTACCGAGTTG | 91.7% | 9185 | Db | 3456 | GCCCTAATCTGCGCGGACCAAAAACCAAGTGAAGGCTCAAGTTGTGCAACTGCTG | 86.6% | 9185 | Db | 3456 | GCCCTAATCTGCGCGGACCAAAAACCAAGTGAAGGCTCAAGTTGTGCAACTGCTG | 86.6% | 9185 | Db | 3456 | GCCCTAATCTGCGCGGACCAAAAACCAAGTGAAGGCTCAAGTTGTGCAACTGCTG | 86.6% | 9185 | Db | 3456 | GCCCTAATCTGCGCGGACCAAAAACCAAGTGAAGGCTCAAGTTGTGCAACTGCTG | 86.6% | 9185 |
| Qy | 2042 | ATGAATGGAAGAGTCT 2059 | 91.7% | 9185 | Qy | 2 | TGGCGCTATGACGCGCTATGCGCGACGACGACGAGGCGCTTTTGGAGTGAATACCA | 86.6% | 9185 | Qy | 2 | TGGCGCTATGACGCGCTATGCGCGACGACGACGAGGCGCTTTTGGAGTGAATACCA | 86.6% | 9185 | Qy | 2 | TGGCGCTATGACGCGCTATGCGCGACGACGACGAGGCGCTTTTGGAGTGAATACCA | 86.6% | 9185 | Qy | 2 | TGGCGCTATGACGCGCTATGCGCGACGACGACGAGGCGCTTTTGGAGTGAATACCA | 86.6% | 9185 |
| Db | 5117 | ATGAGATGGAAGAGTCT 5134 | 91.7% | 9185 | Db | 3396 | TGGCGCCCATCACGCGCGTACGCGCCACGACGACCAAGGCGCTCTTAAGGTCATTAATCACCA | 86.6% | 9185 | Db | 3396 | TGGCGCCCATCACGCGCGTACGCGCCACGACGACCAAGGCGCTCTTAAGGTCATTAATCACCA | 86.6% | 9185 | Db | 3396 | TGGCGCCCATCACGCGCGTACGCGCCACGACGACCAAGGCGCTCTTAAGGTCATTAATCACCA | 86.6% | 9185 | Db | 3396 | TGGCGCCCATCACGCGCGTACGCGCCACGACGACCAAGGCGCTCTTAAGGTCATTAATCACCA | 86.6% | 9185 |
| <p>RESULT 14</p> <p>US-08-444-818-122</p> <p>Sequence 122, Application US/08444818</p> <p>Patent No. 6150087</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: Chien, David Y.</p> <p>APPLICANT: Rutter, William J.</p> <p>TITLE OF INVENTION: NANV Diagnostics and Vaccines</p> <p>NUMBER OF SEQUENCES: 777</p> <p>CORRESPONDENCE ADDRESS:</p> <p>ADDRESSEE: Chiron Corporation</p> <p>STREET: 4560 Horton Street</p> <p>CITY: Emeryville</p> <p>STATE: CA</p> <p>COUNTRY: USA</p> <p>ZIP: 94608-2916</p> <p>COMPUTER READABLE FORM:</p> <p>MEDIUM TYPE: Floppy disk</p> <p>COMPUTER: IBM PC compatible</p> <p>OPERATING SYSTEM: PC-DOS/MS-DOS</p> <p>SOFTWARE: Patentin Release #1.0, Version #1.30</p> <p>CURRENT APPLICATION DATA:</p> <p>APPLICATION NUMBER: US/08/444,818</p> <p>FILING DATE:</p> <p>CLASSIFICATION: 424</p> <p>PRIOR APPLICATION DATA:</p> <p>APPLICATION NUMBER: US/08/403,590</p> <p>FILING DATE: 14-MAR-1995</p> <p>ATTORNEY/AGENT INFORMATION:</p> <p>NAME: Harbin, Alisa A.</p> <p>REGISTRATION NUMBER: 33,895</p> <p>REFERENCE/DOCKET NUMBER: 0110, 002</p> <p>TELECOMMUNICATION INFORMATION:</p> <p>TELEPHONE: (508)359-3876</p> <p>TELEFAX: (508)359-3885</p> <p>INFORMATION FOR SEQ ID NO: 122:</p> <p>SEQUENCE CHARACTERISTICS:</p> <p>LENGTH: 9185 base pairs</p> <p>TYPE: nucleic acid</p> <p>STRANDEDNESS: single</p> <p>TOPOLOGY: linear</p> <p>MOLECULE TYPE: cDNA</p> <p>US-08-444-818-122</p> | | | | | | | | | | | | | | | | | | | | | | | | |
| <p>Query Match</p> <p>Best Local Similarity 91.7%; Pred. No. 0;</p> <p>Matches 1887; Conservative 0; Mismatches 171; Indels 0; Gaps 0;</p> | | | | | | | | | | | | | | | | | | | | | | | | |

Db 3576 GAAAGAGGACATCGGTCACCCAGAGGCTCTGTATCCAGATGATACCAATGTAAGACC 3635
Qy 242 AAGACTCGTAGGCTGGCCCGCTCCCAAGGTGCCGCTCATTAACCATGCACTTGGC 301
Db 3636 AAGACTTGTGGCTGGCCCGCTCCCAAGGTAGCGCTCATTTGACACCTTGCACTTGGC 3695
Qy 302 GCTCTCGGACCTTAACCTGTGACAGAGGACCGGATGTCATCTGTGGCCGACCGG 361
Db 3636 GCTCTCGGACCTTAACCTGTGACAGAGGACCGGATGTCATCTGTGGCCGACCGG 3755
Qy 362 GTGATGGAGGGGACCGCTGCTTGGCCCGGCTATCTTACTTGAAGGCTCTCGG 421
Db 3756 GTGATAGAGGGGACCGCTGCTGTGGCCCGGCTATCTTACTTGAAGGCTCTCGG 3815
Qy 422 GAGGCCCTGCTGTGGCCCGGACGACATGCGGTAGGCAATTGAGCGCGGTATGCA 481
Db 3816 GGGGTCCGCTGTGTGGCCCGGAGGACGCGGTGGGCATATTTAGGGCCGCGGTGCA 3875
Qy 482 CCCGTGAGTGGCTAAGGGGCGTGAATTGATCCCGTGAAGGCTTGAAGCAACATGA 541
Db 3876 CCCGTGAGTGGCTAAGGGGCGTGAATTGATCCCGTGAAGGCTTGAAGCAACATGA 3935
Qy 542 GGTCCCGGTGTTCTCAGACAACTCTCCCAAGAGTGCCTGAGCTACCAAGTGG 601
Db 3936 GGTCCCGGTGTTCAAGGATGCTCTCTCCCAAGAGTGCCTGAGCTACCAAGTGG 3995
Qy 602 CCCACCTGATGCTCCCAAGGCGAGGCGGTGAAGACCAAGGTCCCGGCGCATAGCAG 661
Db 3996 CTCACCTTCATGCTCCCAAGGCGAGGCGGCAAAAGCAACCAAGGTCCCGGCGCATAGCAG 4055
Qy 662 CTCAGGGCTACAAGGCTGTGCTCAACCCCTCGGTGCTGCACAATGGGCTTGTGG 721
Db 4056 CTCAGGGCTAATAGGCTAATGATCTCAACCCCTCGGTGCTGCACAATGGGCTTGTGG 4115
Qy 722 CTTATAGTCCAAAGGCCCATGAGATTGATCTTACATCAGAGCTGGGGTGAAGCAATTA 781
Db 4116 CTTATAGTCCAAAGGCTCATGGGATGATCTTACATCAGAGCCGGGGTGAAGCAATTA 4175
Qy 782 CTATGAGAGCCCGATCAACGTAATTCACCTACGAGGATTCCTTGGCCAGCGGGGTGT 841
Db 4176 CCAGTGGAGGCCCATCACTGCTCAACCTACGAGGATTCCTTGGCCAGCGGGGTGT 4235
Qy 842 CAGGGGGTCTATATACATTAATTGTGACGAGTGCATCTCAACGATGCAATCA 901
Db 4236 CAGGGGGTCTATATACATTAATTGTGACGAGTGCATCTCAACGATGCAATCA 4295
Qy 902 TCTTGGGATTTGGCACTGCTCTTGAACCAAGCAGAGACCGGGGGCGAGACTGACTGTC 961
Db 4296 TCTTGGGATTCGGCACTGCTCTTGAACCAAGCAGAGACTGCGGGGCGAGACTGCTGTC 4355
Qy 962 TCGCCACCGCTACCCCTCGGGGCTCGTCACTGTGTGCCCATCTTAACATGAGAGTTG 1021
Db 4356 TCGCCACCGCTACCCCTCGGGGCTCGTCACTGTGTGCCCATCTTAACATGAGAGTTG 4415
Qy 1022 CTCTGTCCATTCACCGGAGAGATCCCTTTTATGGCAAGGCTATTCCTTGAAGCAATTA 1081
Db 4416 CTCTGTCCATTCACCGGAGAGATCCCTTTTATGGCAAGGCTATTCCTTGAAGCAATTA 4475
Qy 1082 AGGGGGGAGACATCTATCTTCTGCACTCAAAAGAGAGTGCAGAGCTGCGCGCA 1141
Db 4476 AGGGGGGAGACATCTATCTTCTGCACTCAAAAGAGAGTGCAGAGCTGCGCGCA 4535
Qy 1142 AACTGTGCGTGGGCGTCAATGCGGTGCTTACTACCGCGGCTTGAATGTGTCTGCA 1201
Db 4536 AACTGTGCGTGGGCGTCAATGCGGTGCTTACTACCGCGGCTTGAATGTGTCTGCA 4595
Qy 1202 TCCGACCAAGTGTGACGTTGTGCTGTGGCAATGACGCGCTCATGACCGGCTTACCG 1261
Db 4596 TCCGACCAAGTGTGACGTTGTGCTGTGGCAATGACGCGCTCATGACCGGCTTACCG 4655
Qy 1262 GCGACTTGATTCGGTGAATGACTGCAACACGTGTGTCACCGAGACAGTTCAGCC 1321

Db 4656 GCGACTTGACTCGGTGATGACTGCAATTAACGTGTGTCACCGAGACAGTTCAGCC 4715
Qy 1322 TTGACCCATACCTTCAACCTTGAACAATCAAGCTTCCCAAGATGCTGTCCGATCTC 1381
Db 4716 TTGACCCATACCTTCAACCTTGAACAATCAAGCTTCCCAAGATGCTGTCCGATCTC 4775
Qy 1382 AACGTGGGGTATGAGACTGGCAGAGGGAAGCAGGATCTAAGATTTGTGGACCGGGG 1441
Db 4776 AACGTGGGGGACAGACTGGCAGGGGGAAGCAGGATCTAAGATTTGTGGACCGGGG 4835
Qy 1442 AGCGTCTTCTGAGCATGTTTGAATCTGTGTCTCTGAGGTCTATAGACGGGGTGTG 1501
Db 4836 AGCGGCTTCCGGGACATGTTTGAATCTGTGTCTCTGAGGTCTATAGACGGGGTGTG 4895
Qy 1502 CTGTGTATGAGCTTACCGCCCGGAGACCAAGTTAAGGCTACAGACATATGAACACC 1561
Db 4896 CTGTGTATGAGCTACCGCCCGGAGACCAAGTTAAGGCTACAGACATATGAACACC 4955
Qy 1562 CCGGACTTCCGGTGTGCAAGACCATCTTGAATTTTGGAGGGCGCTTTACGGGTCTCA 1621
Db 4956 CCGGCTTCCGGTGTGCAAGACCATCTTGAATTTTGGAGGGCGCTTTACAGGCTCA 5015
Qy 1622 CCCACATAGACGCCCATCTTCTATCCAGACAAAGCAGAGTGGGAAAACTTCCCTATC 1681
Db 5016 CTATATATGATGCCCATCTTCTATCCAGACAAAGCAGAGTGGGAAAACTTCCCTATC 5075
Qy 1682 TGTAGCGTACCAAGCACCGGTGTGCTAGAGCTCAAGCCCTCCCTGCTGTGGAGCC 1741
Db 5076 TGTAGCGTATCAAGCACCGGTGTGCTAGAGCTCAAGCCCTCCCTGCTGTGGAGCC 5135
Qy 1742 AGATGTGAAGTGTGATTCGCTCAAGCCCATCTCATAGGCGCAACCTCTGCTAT 1801
Db 5136 AGATGTGAAGTGTGATTCGCTCAAGCCCATCTCATAGGCGCAACCTCTGCTAT 5195
Qy 1802 ATGACTGGGCGCTGTCCAGATGAATGATCACCTGACGACCCAGTCAACATATCA 1861
Db 5196 ATGACTGGGCGCTGTTCAGATGAATGATCACCTGACGACCCAGTCAACATATCA 5255
Qy 1862 TGACATGATGTGCGCTGACCTGAGAGTGTGTCAGAGTAACTTGGGTCTGTGGCGCG 1921
Db 5256 TGACATGATGTGCGCTGACCTGAGAGTGTGTCAGAGTAACTTGGGTCTGTGGCGCG 5315
Qy 1922 TTCTGCTGCTTTGGCGCGGATTTGCTATTCACAGGCTGCTGTATAGGATAGGA 1981
Db 5316 TTCTGCTGCTTTGGCGCGGATTTGCTATTCACAGGCTGCTGTATAGGATAGGA 5375
Qy 1982 TTGCTTGTCCGAAAGCGGCAATCATCCGACAGGAAATCTCTTACCGGAGTTG 2041
Db 5376 TGTCTTGTCCGGAAGCGGCAATCATCCGACAGGAAATCTCTTACCGGAGTTG 5435
Qy 2042 ATGAATGGAAGTGTCT 2059
Db 5436 ATGAATGGAAGTGTCT 5453

RESULT 15
US-08-444-818-123/c
; Sequence 123, Application US/08444818
; Patent No. 6150087
; GENERAL INFORMATION:
; APPLICANT: Chien, David Y.
; APPLICANT: Ruter, William J.
; TITLE OF INVENTION: NANBV Diagnostics and Vaccines
; NUMBER OF SEQUENCES: 777
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,818
FILING DATE:
CLASSIFICATION: 424
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/08/403,590
FILING DATE: 14-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Harbin, Alisa A.
REGISTRATION NUMBER: 33,895
REFERENCE/DOCKET NUMBER: 0110.002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 359-3876
TELEFAX: (508) 359-3885
INFORMATION FOR SEQ ID NO: 123:
SEQUENCE CHARACTERISTICS:
LENGTH: 9185 base pairs
TYPE: nucleic acid
STRADEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ANTI-SENSE: YES
US-08-444-818-123

Query Match 86.6%; Score 1784.4; DB 3; Length 9185;
Best Local Similarity 91.7%; Pred. No. 0;
Matches 1887; Conservative 0; Mismatches 171; Indels 0; Gaps 0;
QY 2 TGGCCGCTATCAGGCTATGCGCCAGACAAAGGGGCTTTGGAGTCAATACCA 61
DB 5790 TGGCGCCATCAGGCGTACGCGACAGACAAAGGGGCTCTAGGGTGCATATACCA 5731
QY 62 GCTTACCGCGCCGAGCAAAAACAAGTGAAGGTGATGATCGTGTCACTGCTG 121
DB 5730 GCTTACGCGCGGAGCAAAAACAAGTGAAGGTGATGATCGATTTGTCACTGCTG 5671
QY 122 CCCAGACTTTCTTGGCAACCTGATTAACGGGGTGTGTGGAAGTCTTACATGAGCCG 181
DB 5670 CCCAAACCTTCTGCGACATGATCAATGGGGTGTGTGGAAGTCTTACATGAGCCG 5611
QY 182 GAACAAGGACATGCGTACCTAAGGGTCTGTTATCCAGATGTAACAATGAGACC 241
DB 5610 GAACAAGGACATGCGTACCTAAGGGTCTGTTATCCAGATGTAACAATGAGACC 5551
QY 242 AAGACTCTGTAAGCTGCGCCGCTCCCAAGTGCCTCATTTAACCCATGACCTTGC 301
DB 5550 AAGACTCTGTAAGCTGCGCCGCTCCCAAGTGCCTCATTTAACCCATGACCTTGC 5491
QY 302 GCTCTCTGGAACCTTTACCTGTGACGAGGACGCGGATGATCTCTGTGCGCGAGG 361
DB 5490 GCTCTCTGGAACCTTTACCTGTGACGAGGACGCGGATGATCTCTGTGCGCGAGG 5431
QY 362 GTGATGGAGGAGGAGCTGTTGGCGCGGCTATCTTACTTGAAGGCTCTCGG 421
DB 5430 GTGATGGAGGAGGAGCTGTTGGCGCGGCTATCTTACTTGAAGGCTCTCGG 5371
QY 422 GAGGCTCTGCTGTGCGCCGAGACATGCGTGAAGCATATTCAGAGCGCGGTATGA 481
DB 5370 GAGGCTCTGCTGTGCGCCGAGAGCATGCGTGAAGCATATTCAGAGCGCGGTATGA 5311
QY 482 CCCGTGAGTGTGAAGCGGTGATCTATCCCGGTAGAGACTTTAGACAAACATCA 541
DB 5310 CCCGTGAGTGTGAAGCGGTGATCTATCCCGGTAGAGACTTTAGACAAACATCA 5251
QY 542 GGTCCCGGTGTCTTCAAGCACTCTCCCAACAGAGTGCCTCAAGACTTCAAGTGG 601
DB 5250 GGTCCCGGTGTCTTCAAGCACTCTCCCAACAGAGTGCCTCAAGACTTCAAGTGG 5191
QY 602 CCCACTGATCTCCCAACGCGAGCGGTGAAGACCAAGGTCCCGGCGGATACGAG 661
DB 5191 CCCACTGATCTCCCAACGCGAGCGGTGAAGACCAAGGTCCCGGCGGATACGAG 661

DB 5190 CTCACTTCATGCTCCCAAGAGAGCAAGCAAAAGACCAAGGTCCCGGCTGATATGAG 5131
QY 662 CTCAAGGCTTCAAGGTGTGTGCTCAACCCCTCGTGTGTGCAACATGGGCTTTGGTG 721
DB 5130 CTCAAGGCTTCAAGGTGTGTGCTCAACCCCTCGTGTGTGCAACATGGGCTTTGGTG 5071
QY 722 CTTCATGTCCAAAGGCCCATGGGATTTGATCTTCAATCAGAGCTGGGGTGAACAATTA 781
DB 5070 CTTCATGTCCAAAGGCCCATGGGATTTGATCTTCAATCAGAGCTGGGGTGAACAATTA 5011
QY 782 CTACTGAGGCGCCGATCAAGTATTCACCTTACCGCAAGTCTTTCGAGCGGGGTGT 841
DB 5010 CCACCTGAGGCGCCGATCAAGTATTCACCTTACCGCAAGTCTTTCGAGCGGGGTGT 4951
QY 842 CAGGGGGTGTATTAACATTAATTTGTGACAGTGCATCCCAAGATGCAATCA 901
DB 4950 CAGGGGGTGTATTAACATTAATTTGTGACAGTGCATCCCAAGATGCAATCA 4891
QY 902 TCTTGGGATTTGGCACTGTCTTGAACAAGACAGACCGCGGGGCGAGACTGATGTC 961
DB 4890 TCTTGGGATTTGGCACTGTCTTGAACAAGACAGACCGCGGGGCGAGACTGATGTC 4831
QY 962 TCGCCACCGCTACCCCTCGGGCTCGTCACTGTGCGCCATCTTAACATCGAGAGTTG 1021
DB 4830 TCGCCACCGCTACCCCTCGGGCTCGTCACTGTGCGCCATCTTAACATCGAGAGTTG 4771
QY 1022 CTCTGTCCATCAGCGGAGAGATCCCTTTTATGGCAAGCTTATTCCTTTGAAGCAATTA 1081
DB 4770 CTCTGTCCATCAGCGGAGAGATCCCTTTTATGGCAAGCTTATTCCTTTGAAGCAATTA 4711
QY 1082 AGGGGGGAGACATCTCTTCTGCACTCAAAAGAAAGTGCAGACAGCTCGCGCA 1141
DB 4710 AGGGGGGAGACATCTCTTCTGCACTCAAAAGAAAGTGCAGACAGCTCGCGCA 4651
QY 1142 AACTGTGCGGTGGGCTCAATGCGGTCTTACTACCGCGGCTTGAATGTGCTGCTCA 1201
DB 4650 AACTGTGCGGTGGGCTCAATGCGGTCTTACTACCGCGGCTTGAATGTGCTGCTCA 4591
QY 1202 TCCCGACAGTGTGACCTTGTGCTGTGGGCACTGAAGCCCTCATGACCGGCTTACG 1261
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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

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Perfect score: 2061
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Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA Main:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 2 | 2061 | 100.0 | 2061 | 3 | US-09-930-591-1 | Sequence 1, Appl |
| 3 | 2061 | 100.0 | 2061 | 6 | US-10-307-047-1 | Sequence 1, Appl |
| 4 | 2061 | 100.0 | 2061 | 8 | US-10-817-591-16 | Sequence 16, Appl |
| 5 | 2061 | 100.0 | 2061 | 10 | US-11-043-808-1 | Sequence 1, Appl |
| 6 | 1786 | 86.7 | 9379 | 3 | US-09-916-359-1 | Sequence 1, Appl |
| 7 | 1786 | 86.7 | 9401 | 7 | US-10-445-724-1 | Sequence 1, Appl |
| 8 | 1781.2 | 86.4 | 2058 | 3 | US-09-881-239-2 | Sequence 2, Appl |
| 9 | 1781.2 | 86.4 | 2058 | 7 | US-10-643-853-2 | Sequence 1, Appl |
| 10 | 1781.2 | 86.4 | 2058 | 7 | US-10-658-782-1 | Sequence 1, Appl |
| 11 | 1779.6 | 86.3 | 2058 | 7 | US-09-881-654-1 | Sequence 1, Appl |
| 12 | 1779.6 | 86.3 | 2058 | 7 | US-10-637-323-1 | Sequence 1, Appl |
| 13 | 1779.6 | 86.3 | 2058 | 8 | US-10-899-715-1 | Sequence 1, Appl |
| 14 | 1774.8 | 86.1 | 12980 | 3 | US-09-238-076-5 | Sequence 5, Appl |
| 15 | 1774.8 | 86.1 | 12980 | 3 | US-09-917-563-5 | Sequence 5, Appl |
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| 18 | 1773.2 | 86.0 | 9646 | 3 | US-09-929-955-16 | Sequence 1, Appl |
| 19 | 1773.2 | 86.0 | 9646 | 3 | US-09-917-563-1 | Sequence 1, Appl |
| 20 | 1765.2 | 85.6 | 10803 | 3 | US-09-189-359-13 | Sequence 13, Appl |
| 21 | 1765.2 | 85.6 | 10803 | 3 | US-09-747-419-17 | Sequence 17, Appl |
| 22 | 1765.2 | 85.6 | 10803 | 6 | US-10-259-275-17 | Sequence 17, Appl |
| 23 | 1765.2 | 85.6 | 10803 | 10 | US-11-006-313-17 | Sequence 17, Appl |

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| 24 | 1762 | 85.5 | 9416 | 3 | US-09-929-955-13 | Sequence 13, Appl |
| 25 | 1762 | 85.5 | 9416 | 5 | US-10-104-966-13 | Sequence 13, Appl |
| 26 | 1762 | 85.5 | 9416 | 7 | US-10-719-619-13 | Sequence 13, Appl |
| 27 | 1762 | 85.5 | 9416 | 8 | US-10-817-591-13 | Sequence 13, Appl |
| 28 | 1757.2 | 85.3 | 9646 | 8 | US-09-742-659-3 | Sequence 1, Appl |
| 29 | 1754 | 85.1 | 6609 | 7 | US-10-475-989-1 | Sequence 1, Appl |
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| 32 | 1752.4 | 85.0 | 3636 | 9 | US-10-939-958-4 | Sequence 4, Appl |
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| 36 | 1749.2 | 84.9 | 9365 | 3 | US-09-827-668-7 | Sequence 7, Appl |
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| 39 | 1557.8 | 75.6 | 2064 | 3 | US-09-884-456-69 | Sequence 69, Appl |
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ALIGNMENTS

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US-09-929-955-16
; Sequence 16, Application US/09929955
; Patent No. US20020136740A1
; GENERAL INFORMATION:
; APPLICANT: Matzi Salberg
; TITLE OF INVENTION: VACCINES CONTAINING RIBAVIRIN AND
; FILE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: TRIPEP.23AUS2
; CURRENT APPLICATION NUMBER: US/09/929,955
; PRIOR FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: 09/705,547
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: 60/229,175
; PRIOR FILING DATE: 2000-08-29
; PRIOR APPLICATION NUMBER: 60/225,767
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 2061
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hepatitis C virus NS3/4A coding region
US-09-929-955-16
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; Publication No. US20040092730A1
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; APPLICANT: Macti Salberg
; TITLE OF INVENTION: A HEPATITIS C VIRUS NON-STRUCTURAL
; FILE REFERENCE: TRIPEP 028AUS
; CURRENT APPLICATION NUMBER: US/09/930,591
; PRIOR APPLICATION NUMBER: 60/225,767
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/229,175
; PRIOR FILING DATE: 2000-08-29
; PRIOR APPLICATION NUMBER: 09/705,547
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; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0

/ SEQ ID NO 1
/ LENGTH: 2061
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Hepatitis C virus NS3/4A coding region
US-09-930-591-1

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Matches 2061; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1741 CAGATGTGAAGTGTGTTAATCCGTCAAGGCCCACTTCAAGGGCAACACTCTGCTA 1800
QY 1801 TATAGACTGGGCGCTGTCCAGATGAAGTCAACCTGACGCAACCCAGTCAACCAATATATC 1860
DB 1801 TATAGACTGGGCGCTGTCCAGATGAAGTCAACCTGACGCAACCCAGTCAACCAATATATC 1860
QY 1861 ATGACATGATGTGCGGCTGACCTGGAAGTCTGACAGATACCTGGGTGCTGTTGGCGGC 1920
DB 1861 ATGACATGATGTGCGGCTGACCTGGAAGTCTGACAGATACCTGGGTGCTGTTGGCGGC 1920
QY 1921 GTTCTGCGCTTGGCGCGGATGCTTATCAAGGCTGCGGTGATGATAGTAGTAG 1980
DB 1921 GTTCTGCGCTTGGCGCGGATGCTTATCAAGGCTGCGGTGATGATAGTAGTAG 1980
QY 1981 ATTGTCTTGTCCGGAACCGGCAATCATATCCGACAGGAGATGCTCTGATCCGGAGTTTC 2040

Db 1981 ATTGCTTGTCGCGAAGAGCCGCGCAATCATCCGACAGGAGAGTCTCTACCGGAGTTTC 2040
QY 2041 GATGAATGGAAGAGTGTGA 2061
Db 2041 GATGAATGGAAGAGTGTGA 2061

RESULT 3
US-10-307-047-1

/ Sequence 1, Application US/10307047
/ Publication No. US20030206919A1
/ GENERAL INFORMATION:
/ APPLICANT: Matci Sallberg
/ TITLE OF INVENTION: A HEPATITIS C VIRUS NON-STRUCTURAL
/ FILE REFERENCE: TRIPEP_028CPI
/ CURRENT APPLICATION NUMBER: US/10/307,047
/ PRIOR FILING DATE: 2002-11-26
/ PRIOR APPLICATION NUMBER: 60/225,767
/ PRIOR FILING DATE: 2000-08-17
/ PRIOR APPLICATION NUMBER: 60/229,175
/ PRIOR FILING DATE: 2000-08-29
/ PRIOR APPLICATION NUMBER: 09/705,547
/ PRIOR FILING DATE: 2000-11-03
/ PRIOR APPLICATION NUMBER: 09/930591
/ PRIOR FILING DATE: 2001-08-15
/ NUMBER OF SEQ ID NOS: 38
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 1
/ LENGTH: 2061
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Hepatitis C virus NS3/4A coding region
US-10-307-047-1

Query Match 100.0%; Score 2061; DB 6; Length 2061;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2061; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGGCGCTTATCAAGGCTTATGCCCCAGACAGAGGGGCTTTTGGAGTGCATTAATCAC 60
Db 1 ATGGGCGCTTATCAAGGCTTATGCCCCAGACAGAGGGGCTTTTGGAGTGCATTAATCAC 60
QY 61 AGCTTGACCGCGCGGGGCAAAAACAGGTGAGGGGTGAGGTTCAATGCTGCACTGCT 120
Db 61 AGCTTGACCGCGCGGGGCAAAAACAGGTGAGGGGTGAGGTTCAATGCTGCTGCTGCT 120
QY 121 GCCCAGACTTTCTTGGCAACTGCAATTAACGGGGTGTGTTGAGACTGTCTACCATGAGCC 180
Db 121 GCCCAGACTTTCTTGGCAACTGCAATTAACGGGGTGTGTTGAGACTGTCTACCATGAGCC 180
QY 181 GGAACAGAGACATTGCGTCACTTAAGGCTCTGTTATCAGATGTAACCAATGTGAC 240
Db 181 GGAACAGAGACATTGCGTCACTTAAGGCTCTGTTATCAGATGTAACCAATGTGAC 240
QY 241 CAAGACTCTGTAGGCTGCGCGCTCCCAAGGTGCGCGCTCATTAACCAATGCACTTGC 300
Db 241 CAAGACTCTGTAGGCTGCGCGCTCCCAAGGTGCGCGCTCATTAACCAATGCACTTGC 300
QY 301 GGCCTCTCGGACCTTTACTGTGTCAAGAGCAAGCGCATGCTCTGTGCGCGAGCC 360
Db 301 GGCCTCTCGGACCTTTACTGTGTGTCAAGAGCAAGCGCATGCTCTGTGCGCGAGCC 360
QY 361 GGTGATGCGAGGGGAGCCTGCTTTGCGCGCGCTTATCTTTACTTGAAGAGCTCTCG 420
Db 361 GGTGATGCGAGGGGAGCCTGCTTTGCGCGCGCTTATCTTTACTTGAAGAGCTCTCG 420
QY 421 GGAAGGCGCTGCTGTGCGCGCGAGAGCAATGCGATGATTAAGAGCGCGGTATGC 480
Db 421 GGAAGGCGCTGCTGTGCGCGCGAGAGCAATGCGATGATTAAGAGCGCGGTATGC 480
QY 481 ACCGCTGAGTGGCTAAGCGGCTGACCTTATCCCGGTAGAGAGCTTGAAGCAACATG 540

Db 481 ACCGCTGAGTGGCTAAGCGGCTGACCTTATCCCGGTAGAGAGCTTGAAGCAACATG 540
QY 541 AGGTCCCGGCTGTTCTAGACAATCTCTCCCAAGAGTGCCTCCAGAGCTACCAAGTG 600
Db 541 AGGTCCCGGCTGTTCTAGACAATCTCTCCCAAGAGTGCCTCCAGAGCTACCAAGTG 600
QY 601 GCCCAGCTGATGCTCCCAAGCGGAGCGGTAAAGACCAAGATCCCGGCGCATACGA 660
Db 601 GCCCAGCTGATGCTCCCAAGCGGAGCGGTAAAGACCAAGATCCCGGCGCATACGA 660
QY 661 GCTCAGGGCTCAAGAGTCTGTGTCAACCCCTCGTTGCTGCAACAATGAGGCTTTGCT 720
Db 661 GCTCAGGGCTCAAGAGTCTGTGTCAACCCCTCGTTGCTGCAACAATGAGGCTTTGCT 720
QY 721 GCTTACATGTCCAAAGGCCATGAGATTGATCTTAATCAGAGACTGGGTGAGCAATT 780
Db 721 GCTTACATGTCCAAAGGCCATGAGATTGATCTTAATCAGAGACTGGGTGAGCAATT 780
QY 781 ACTACTGCGAGCGCGATCAGCAATTCACCTACGCGCAAGTTCTTGCCGACGCGGAGT 840
Db 781 ACTACTGCGAGCGCGATCAGCAATTCACCTACGCGCAAGTTCTTGCCGACGCGGAGT 840
QY 841 TCAGGGGTGCTTATGACATTAATTTGTGACAGTGCACCTCCAGATGCAATCC 900
Db 841 TCAGGGGTGCTTATGACATTAATTTGTGACAGTGCACCTCCAGATGCAATCC 900
QY 901 ATCTTGGGCAATTTGGCACTGTCTTGAACAGACAGACCGGGGGCGAGACTGCTGTG 960
Db 901 ATCTTGGGCAATTTGGCACTGTCTTGAACAGACAGACCGGGGGCGAGACTGCTGTG 960
QY 961 CTCGCGCACCGCTACCCCTCCGGGCTCCGTCACTGTCGCCCACTCTTAATCAGAGAGTT 1020
Db 961 CTCGCGCACCGCTACCCCTCCGGGCTCCGTCACTGTCGCCCACTCTTAATCAGAGAGTT 1020
QY 1021 GCTCTGTCACCTTACCGAGAGATCCCTTTATGCGAAGCTATTCCCTTGAGCAATT 1080
Db 1021 GCTCTGTCACCTTACCGAGAGATCCCTTTATGCGAAGCTATTCCCTTGAGCAATT 1080
QY 1081 AAGGGGGGGAACATCTTATCTTGTGCACTCAAGAAAGAAAGTGGAGAGCTCCCGCA 1140
Db 1081 AAGGGGGGGAACATCTTATCTTGTGCACTCAAGAAAGAAAGTGGAGAGCTCCCGCA 1140
QY 1141 AAACGTGTGCGGTTGGGCGTCAATGCGGTGCTTACTACCGGCGCTTGATGTCCGTC 1200
Db 1141 AAACGTGTGCGGTTGGGCGTCAATGCGGTGCTTACTACCGGCGCTTGATGTCCGTC 1200
QY 1201 ATCCGACCAATGTGACGTTGTGCTGTGCAACTGACGCGCTCATGACCGGCTTTAGC 1260
Db 1201 ATCCGACCAATGTGACGTTGTGCTGTGCAACTGACGCGCTCATGACCGGCTTTAGC 1260
QY 1261 GGGCAGCTTCAATGCGGTATGACATGCAACAGGTGTGACCAACAGTGCACCTTCAGC 1320
Db 1261 GGGCAGCTTCAATGCGGTATGACATGCAACAGGTGTGACCAACAGTGCACCTTCAGC 1320
QY 1321 CTGACCTTACTTACCATTTGAGACATCAAGCTTCCCAAGAGTGTCTCCGTAAT 1380
Db 1321 CTGACCTTACTTACCATTTGAGACATCAAGCTTCCCAAGAGTGTCTCCGTAAT 1380
QY 1381 CAACGTCGGGGTGAAGCTTGCAAGAGGAAGCCAGGCAATCTACAGTTTGTGCAACG 1440
Db 1381 CAACGTCGGGGTGAAGCTTGCAAGAGGAAGCCAGGCAATCTACAGTTTGTGCAACG 1440
QY 1441 GAGGCTCTTCTGTGAGATTTGACTGCTGTCTCTGTCGAGTGTATAGCGCGGTTGT 1500
Db 1441 GAGGCTCTTCTGTGAGATTTGACTGCTGTCTCTGTCGAGTGTATAGCGCGGTTGT 1500
QY 1501 GCTTGTATGAGCTTACCGCGCGAGACCAAGTTAGGCTACAGACATACATGAACCC 1560
Db 1501 GCTTGTATGAGCTTACCGCGCGAGACCAAGTTAGGCTACAGACATACATGAACCC 1560
QY 1561 CCGGAGCTTCCCGGTGCAAGAACCATCTTGAATTTTGGAGGGGCTTTTACGGGCTTC 1620

Db 1561 CCGGACCTTCCCGTGTGCGCAAGACCATCTTGAATTTGGAGGCGCTCTTACCGGGCTTC 1620
Qy 1621 ACCCATATAGAGCCCACTTCTATCCAGACAAAGCAGAGTGGGAAAACTTCCCTAT 1680
Db 1621 ACCCATATAGAGCCCACTTCTATCCAGACAAAGTGGGAAAACTTCCCTAT 1680
Qy 1681 CTGTGAGCGTACCAAGCCACCGTGTGCGTGAAGCTCAAGCCCTCCCGCTGTGGAC 1740
Db 1681 CTGTGAGCGTACCAAGCCACCGTGTGCGTGAAGCTCAAGCCCTCCCGCTGTGGAC 1740
Qy 1741 CAGATGTGGAAGTGTGATCCGCTCTCAAGCCCACTTCATGGCCAAACCTCTGTCTA 1800
Db 1741 CAGATGTGGAAGTGTGATCCGCTCTCAAGCCCACTTCATGGCCAAACCTCTGTCTA 1800
Qy 1801 TATATACCTGGGCGCTGTCCAGATGAAGTCAACCTTCAGCCCACTTCATGGCCAAACCTCTGTCTA 1860
Db 1801 TATATACCTGGGCGCTGTCCAGATGAAGTCAACCTTCAGCCCACTTCATGGCCAAACCTCTGTCTA 1860
Qy 1861 ATGACATGTATGTCCGCTGACCTGAGAGTGTCTACAGAGTACCTGGGCTGTGGAGG 1920
Db 1861 ATGACATGTATGTCCGCTGACCTGAGAGTGTCTACAGAGTACCTGGGCTGTGGAGG 1920
Qy 1921 GTTGTGCTGCTTTGGCGCGGATGATGCTATCCAGAGCTGTGGCTCATAGAGTGA 1980
Db 1921 GTTGTGCTGCTTTGGCGCGGATGATGCTATCCAGAGCTGTGGCTCATAGAGTGA 1980
Qy 1981 ATTGTCTGTCCGGAAGCCCGCATCATACCCGACAGGAGTCTCTACCGGAGTTTC 2040
Db 1981 ATTGTCTGTCCGGAAGCCCGCATCATACCCGACAGGAGTCTCTACCGGAGTTTC 2040
Qy 2041 GATGAATGGAAGAGTGTCTGA 2061
Db 2041 GATGAATGGAAGAGTGTCTGA 2061

RESULT 4
US-10-817-591-16
; Sequence 16, Application US/10817591
; Publication No. US20040229832A1
; GENERAL INFORMATION:
; APPLICANT: Matti Sallberg
; APPLICANT: Catharina Hultgren
; TITLE OF INVENTION: VACCINES CONTAINING RIBAVIRIN AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: TRIPEP 23AUS2c1
; CURRENT APPLICATION NUMBER: US/10/817,591
; PRIOR FILING DATE: 2004-04-02
; PRIOR APPLICATION NUMBER: 10/719,619
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 10/104,966
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 09/929,955
; PRIOR FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: 09/705,547
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: 60/229,175
; PRIOR FILING DATE: 2000-08-29
; PRIOR APPLICATION NUMBER: 60/225,767
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 16
; LENGTH: 2061
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hepatitis C virus NS3/4A coding region
US-10-817-591-16

Query Match 100.0%; Score 2061; DB 8; Length 2061;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2061; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGCCCTATACAGGCTTATGCCCCAGAGACAAAGGCGCTTTGGAGTGCATTAACACC 60
Db 1 ATGGGCGCTATACAGGCTTATGCCCCAGAGACAAAGGCGCTTTGGAGTGCATTAACACC 60
Qy 61 AGCTTGACCGGCGGGAACAAAACAGGTGAGGTGAGTTCAATGTGTCAACTGCT 120
Db 61 AGCTTGACCGGCGGGAACAAAACAGGTGAGGTGAGTTCAATGTGTCAACTGCT 120
Qy 121 GCCCAGACTTTCTTGGCAACCTGCAATTAACGGGGGTGTGAGACTGTCAATGAGAGCC 180
Db 121 GCCCAGACTTTCTTGGCAACCTGCAATTAACGGGGGTGTGAGACTGTCAATGAGAGCC 180
Qy 181 GGAACAGAACCAATGCTCACTTAAGGATCTGTATCAAGATGACCAATGTGAC 240
Db 181 GGAACAGAACCAATGCTCACTTAAGGATCTGTATCAAGATGACCAATGTGAC 240
Qy 241 CAAGAAGCTGTAGAGGTGCGCTCCCAAGGTGCGGCTCATTTAACACATGCACTTGC 300
Db 241 CAAGAAGCTGTAGAGGTGCGCTCCCAAGGTGCGGCTCATTTAACACATGCACTTGC 300
Qy 301 GGTCTCTGGAACCTTTACTGTGTCAAGAGGACCGGATGATCTGTGCGGCGGAGG 360
Db 301 GGTCTCTGGAACCTTTACTGTGTCAAGAGGACCGGATGATCTGTGCGGCGGAGG 360
Qy 361 GGTCTCTGGAACCTTTACTGTGTCAAGAGGACCGGATGATCTGTGCGGCGGAGG 420
Db 361 GGTCTCTGGAACCTTTACTGTGTCAAGAGGACCGGATGATCTGTGCGGCGGAGG 420
Qy 421 GGAAGGCGCTTGTGTGCTGCTCCGACAGACATGCGGTATGAGAGCGGCTATGC 480
Db 421 GGAAGGCGCTTGTGTGCTGCTCCGACAGACATGCGGTATGAGAGCGGCTATGC 480
Qy 481 ACCGTGAGAGTGTGCTTAAGGCGGTGATCTTCAATCCCGTGAAGAGTGTGAGCAACCATG 540
Db 481 ACCGTGAGAGTGTGCTTAAGGCGGTGATCTTCAATCCCGTGAAGAGTGTGAGCAACCATG 540
Qy 541 AGGTCCCGGCTGTCTCAGACAACTCTCCACAGAGTGCAGAGTGCAGAGTGCAGAGTGC 600
Db 541 AGGTCCCGGCTGTCTCAGACAACTCTCTCCACAGAGTGCAGAGTGCAGAGTGCAGAGTGC 600
Qy 601 GCCCAGCTGATGCTCCCAACCGGACGGGTAAAGACCAAGGTCCCGGCGCATACGCA 660
Db 601 GCCCAGCTGATGCTCCCAACCGGACGGGTAAAGACCAAGGTCCCGGCGCATACGCA 660
Qy 661 GCTCAGGCTACAGAGTGTGTGTCTCAACCTCCGTGCTGCAACAATGGGCTTTGCT 720
Db 661 GCTCAGGCTACAGAGTGTGTGTCTCAACCTCCGTGCTGCAACAATGGGCTTTGCT 720
Qy 721 GCTTACATGTCCAAAGGCCATGAGATGATCTTACATCAGAGTGGGCTGAGCAAT 780
Db 721 GCTTACATGTCCAAAGGCCATGAGATGATCTTACATCAGAGTGGGCTGAGCAAT 780
Qy 781 ACTACTGACAGCCGATCAAGTATCACTCAAGCAAGTCTTGGCGAGCGGGTGT 840
Db 781 ACTACTGACAGCCGATCAAGTATCACTCAAGCAAGTCTTGGCGAGCGGGTGT 840
Qy 841 TCAAGGCGGTGCTTAAGACATTAATTTGTGACAGAGTGCCTCAAGAGTGCATTC 900
Db 841 TCAAGGCGGTGCTTAAGACATTAATTTGTGACAGAGTGCCTCAAGAGTGCATTC 900
Qy 901 ATCTGGGCAATGGACATGTCTTGAACCAAGAGAGACCGGGGGGCGAGACTGAG 960
Db 901 ATCTGGGCAATGGACATGTCTTGAACCAAGAGAGACCGGGGGGCGAGACTGAG 960
Qy 961 CTGCGCACCGTACCCCTCCGGGCTCGGTCACTGTGCCCCATCTTAATCAGAGAGTT 1020
Db 961 CTGCGCACCGTACCCCTCCGGGCTCGGTCACTGTGCCCCATCTTAATCAGAGAGTT 1020
Qy 1021 GCTCTGTCACTACCGAGAGATTCCTTTTATGGAAGGCTATTCCTCTTGAACCAAT 1080
Db 1021 GCTCTGTCACTACCGAGAGATTCCTTTTATGGAAGGCTATTCCTCTTGAACCAAT 1080
Qy 1081 AAGGGGGGAGACATCTATCTTGTGCACTCAAGAGAGAGTGCAGAGCTCGCGCA 1140

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Db 1081 AAGGGGGGAGACATCTCATCTTCTGCCACTCAAGAAAGAGTGGAGAGCTCCCGCA 1140
Qy 1141 AAACGTGTGCGTGTGGGCGTCAATGCCGTGCTTACTACCGGGGCTTATGTGTCCGTC 1200
Db 1141 AAACGTGTGCGTGTGGGCGTCAATGCCGTGCTTACTACCGGGGCTTATGTGTCCGTC 1200
Qy 1201 ATCCGACAGTGTGACGTGTGCGTGTGGCACTGACGCGCTCATGACCGGCTTTACC 1260
Db 1201 ATCCGACAGTGTGACGTGTGCGTGTGGCACTGACGCGCTCATGACCGGCTTTACC 1260
Qy 1261 GCGCATTTGATTCGCTGTGATAGACTGCAACAGTGTGTCAACCAAGTGTGATTCAGC 1320
Db 1261 GCGCATTTGATTCGCTGTGATAGACTGCAACAGTGTGTCAACCAAGTGTGATTCAGC 1320
Qy 1321 CTGTGACCTTCACTTCACTTGAAGACATCAAGCTTCCCAAGATGCTGTCCGCTACT 1380
Db 1321 CTGTGACCTTCACTTCACTTGAAGACATCAAGCTTCCCAAGATGCTGTCCGCTACT 1380
Qy 1381 CAACGTGCGGGGTAGGACTGCGAGAGGGAAGCCAGGACTTACAGATTGTGGACCGGGG 1440
Db 1381 CAACGTGCGGGGTAGGACTGCGAGAGGGAAGCCAGGACTTACAGATTGTGGACCGGGG 1440
Qy 1441 GAGCGTCTTCTGCGCATGTTTTGACTCTGCTGTCTCTGCGAGTGTATGACGCGGTTGT 1500
Db 1441 GAGCGTCTTCTGCGCATGTTTTGACTCTGCTGTCTCTGCGAGTGTATGACGCGGTTGT 1500
Qy 1501 GCTTGTGTATGAGCTTACGCCCCCGAGACACAGTTAAGCTTACAGCATACATGAACACC 1560
Db 1501 GCTTGTGTATGAGCTTACGCCCCCGAGACACAGTTAAGCTTACAGCATACATGAACACC 1560
Qy 1561 CCGGGGACTTCCCGGTGTGCGCAAGACCATCTTGAATTTTGGAGAGGCGCTTTTACGGGTC 1620
Db 1561 CCGGGGACTTCCCGGTGTGCGCAAGACCATCTTGAATTTTGGAGAGGCGCTTTTACGGGTC 1620
Qy 1621 ACCCATATGAGCGCCCATCTTCTATCCAGACAAAGACAGTGGGAAAACTTCCCTAT 1680
Db 1621 ACCCATATGAGCGCCCATCTTCTATCCAGACAAAGACAGTGGGAAAACTTCCCTAT 1680
Qy 1681 CTGTGTGCTTACCAAGCCACCGTGTGCGTAAAGCTCAAGCCCTTCCCGTGTGGAGC 1740
Db 1681 CTGTGTGCTTACCAAGCCACCGTGTGCGTAAAGCTCAAGCCCTTCCCGTGTGGAGC 1740
Qy 1741 CAGATGTGAAAGTGTGTATGCTGTCAAGCCCACTTCATGTGGGCAACCTCTGTCTA 1800
Db 1741 CAGATGTGAAAGTGTGTATGCTGTCAAGCCCACTTCATGTGGGCAACCTCTGTCTA 1800
Qy 1801 TATAGACTGGGCGCTGTCCAGATGAAGTCACTCTGACGCAACCACTCAAGATATATC 1860
Db 1801 TATAGACTGGGCGCTGTCCAGATGAAGTCACTCTGACGCAACCACTCAAGATATATC 1860
Qy 1861 ATGACATGTATGTGCGGTGACCTGTGAGGTGTGTCAAGAGTACTGGGTGTCTGTGGCGGC 1920
Db 1861 ATGACATGTATGTGCGGTGACCTGTGAGGTGTGTCAAGAGTACTGGGTGTCTGTGGCGGC 1920
Qy 1921 GTTCTGCGTGTGTGCGCGGTATGCTATCCAGACAGGCTGTGTGTCTATAGAGGTAG 1980
Db 1921 GTTCTGCGTGTGTGCGCGGTATGCTATCCAGACAGGCTGTGTGTCTATAGAGGTAG 1980
Qy 1981 ATTGTCTTGTCCGAAAGCCGCAATCATACCGACAGGGAAGTCTTACCGGAGTTTC 2040
Db 1981 ATTGTCTTGTCCGAAAGCCGCAATCATACCGACAGGGAAGTCTTACCGGAGTTTC 2040
Qy 2041 GATGAATGAAAGAGTGTCTGA 2061
Db 2041 GATGAATGAAAGAGTGTCTGA 2061
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RESULT 5
US-11-043-808-1
; Sequence 1, Application US/11043808
; Publication No. US20050124573A1
; GENERAL INFORMATION:

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APPLICANT: Macti Salberg  
; TITLE OF INVENTION: A HEPATITIS C VIRUS CODON OPTIMIZED  
; FILE OF INVENTION: NON-STRUCTURAL NS3/4A FUSION GENE  
; FILE REFERENCE: TRIPEP.028CPIC1  
; CURRENT FILING DATE: 2005-01-25  
; PRIOR APPLICATION NUMBER: US/11/043,808  
; PRIOR FILING DATE: 2002-11-26  
; PRIOR APPLICATION NUMBER: 10/307,047  
; PRIOR FILING DATE: 2001-08-15  
; PRIOR APPLICATION NUMBER: 09/929,955  
; PRIOR FILING DATE: 2001-08-15  
; PRIOR APPLICATION NUMBER: 09/930,591  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/225,767  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/229,175  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO: 1  
; LENGTH: 2061  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Hepatitis C virus NS3/4A coding region  
US-11-043-808-1
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Query Match 100.0%; Score 2061; DB 10; Length 2061;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2061; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 ATGGGCGCTTATCAGGCGCTATGCGCAGACAGCAAGGGGCTTTGGAGTCAATATCAC 60
Db 1 ATGGGCGCTTATCAGGCGCTATGCGCAGACAGCAAGGGGCTTTGGAGTCAATATCAC 60
Qy 61 AGCTTGACCGGCGGGGACAAAAACAGGTGAGGTGAGTTCAATCGTGTCAACTGCT 120
Db 61 AGCTTGACCGGCGGGGACAAAAACAGGTGAGGTGAGTTCAATCGTGTCAACTGCT 120
Qy 121 GCCGACTTTCTTGGCACTGTCACTTAAACGGGAGTGTGTGACTGTCTTACATGAGGCC 180
Db 121 GCCGACTTTCTTGGCACTGTCACTTAAACGGGAGTGTGTGACTGTCTTACATGAGGCC 180
Qy 181 GGAACAAGACCATTTGCTGCTACCTTAAGGCTCTGTTATCCAGATGACACCAATGTGAC 240
Db 181 GGAACAAGACCATTTGCTGCTACCTTAAGGCTCTGTTATCCAGATGACACCAATGTGAC 240
Qy 241 CAAGACTCTGTAGGCTGCGCTCCCAAGGTGCCGCTCAATTAACCATGACATTC 300
Db 241 CAAGACTCTGTAGGCTGCGCTCCCAAGGTGCCGCTCAATTAACCATGACATTC 300
Qy 301 GGCTCTTGTGACCTTACCTGTGTCAAGAGGACGCGCATGTATTCCTGTGCGGACGG 360
Db 301 GGCTCTTGTGACCTTACCTGTGTCAAGAGGACGCGCATGTATTCCTGTGCGGACGG 360
Qy 361 GGTGATGAGGAGGAGGAGGCTGTTTGGCGCGGCTTACTCTTACTTGAAGAGTCTCTG 420
Db 361 GGTGATGAGGAGGAGGAGGCTGTTTGGCGCGGCTTACTCTTACTTGAAGAGTCTCTG 420
Qy 421 GGAGGCGCTTGTCTGTGCGCGCAGAGATGCGGTGAGCATATTAAGAGCGCGGTATGC 480
Db 421 GGAGGCGCTTGTCTGTGCGCGCAGAGATGCGGTGAGCATATTAAGAGCGCGGTATGC 480
Qy 481 ACCGTGAGTGTGCTAAGCGGTGTGACTTCAATCCCGTGAAGAGCTTGAAGACCAATG 540
Db 481 ACCGTGAGTGTGCTAAGCGGTGTGACTTCAATCCCGTGAAGAGCTTGAAGACCAATG 540
Qy 541 AGGTCCCGGAGTGTCTCAGACAACTCTCCCAAGAGAGGCGCCAGAGCTACCAAGTG 600
Db 541 AGGTCCCGGAGTGTCTCAGACAACTCTCTCCCAAGAGAGGCGCCAGAGCTACCAAGTG 600
Qy 601 GCCCACTGATGTCTCCACCGGCAAGCGGTGAAGACCAAGGTCCCGGCGCATACGCA 660
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Db 601 GCCGACCTGCAATGCTCCGACGGGCGAGCGGTAAAGACCAAGATCCCGGCGCATACCA 660
Qy 661 GCTCAGGGCTACAAAGTGTGTGTCTCAACCCCTCCGTTGTGCAACAATGGGCTTTGGT 720
Db 661 GCTCAGGGCTACAAAGTGTGTGTCTCAACCCCTCCGTTGTGCAACAATGGGCTTTGGT 720
Qy 721 GCTTACATGTCCAAAGGGCCATGGGATTTAGTCTTACATCAGGACTGGGGGTGAGCAAT 780
Db 721 GCTTACATGTCCAAAGGGCCATGGGATTTAGTCTTACATCAGGACTGGGGGTGAGCAAT 780
Qy 781 ACTACTGGCAGCCCGCATCAGATTTCAACTACGGCAAGTTCTTTCCGACGGCGGATGT 840
Db 781 ACTACTGGCAGCCCGCATCAGATTTCAACTACGGCAAGTTCTTTCCGACGGCGGATGT 840
Qy 841 TCAGGGGGTGTCTTATGACATTAATTTGTGACAGTGTCCACTCCAGGATGCAATCC 900
Db 841 TCAGGGGGTGTCTTATGACATTAATTTGTGACAGTGTCCACTCCAGGATGCAATCC 900
Qy 901 ATCTTGGGCAATTGGCACTGTCTCTTGAACAAGCAGACCGGGGGGCGAGACTGCTGG 960
Db 901 ATCTTGGGCAATTGGCACTGTCTCTTGAACAAGCAGACCGGGGGGCGAGACTGCTGG 960
Qy 961 CTCGCGACCGGTACCCCTCCGGGCTCCGTCACTGTGCCCATCTTAACATGAGGAGTT 1020
Db 961 CTCGCGACCGGTACCCCTCCGGGCTCCGTCACTGTGCCCATCTTAACATGAGGAGTT 1020
Qy 1021 GCTCTGTCACTACCGGAGAGATCCCTTTTATGGCAAGGCTATTCCTTGAAGCAAT 1080
Db 1021 GCTCTGTCACTACCGGAGAGATCCCTTTTATGGCAAGGCTATTCCTTGAAGCAAT 1080
Qy 1081 AAGGGGGGAGACATCTCATCTTCCGACCTCAAGAAAGAGTGGAGAGAGTGGCGCA 1140
Db 1081 AAGGGGGGAGACATCTCATCTTCCGACCTCAAGAAAGAGTGGAGAGAGTGGCGCA 1140
Qy 1141 AAACCTGTGCGGTTGGGCGTCAATGCGGTGCTTACTACCGGGGCTTGAATGTCCGTC 1200
Db 1141 AAACCTGTGCGGTTGGGCGTCAATGCGGTGCTTACTACCGGGGCTTGAATGTCCGTC 1200
Qy 1201 ATCCGACAGTGTGACGTTGTCTGTGCACTGACAGCGCCCTCATACCGGCTTTAC 1260
Db 1201 ATCCGACAGTGTGACGTTGTCTGTGCACTGACAGCGCCCTCATACCGGCTTTAC 1260
Qy 1261 GGGGACCTTGATGGGTATGACGCAACGCTGTCAACCCAGACAGTGGACTTCAGC 1320
Db 1261 GGGGACCTTGATGGGTATGACGCAACGCTGTCAACCCAGACAGTGGACTTCAGC 1320
Qy 1321 CTGACCCCTTACCTTACCATTTGAGACATCAAGCTTCCCGAGAGTGTCTCCGTAAT 1380
Db 1321 CTGACCCCTTACCTTACCATTTGAGACATCAAGCTTCCCGAGAGTGTCTCCGTAAT 1380
Qy 1381 CAACGTCGGGGTGAAGCTGGCAGAGGAAAGCCAGGATCTACAGATTTGTGACCGGG 1440
Db 1381 CAACGTCGGGGTGAAGCTGGCAGAGGAAAGCCAGGATCTACAGATTTGTGACCGGG 1440
Qy 1441 GAGGCTCTTCTGGGATGTTGACTGTCTGTCTCTGAGATGCTAAGACGGGGTGT 1500
Db 1441 GAGGCTCTTCTGGGATGTTGACTGTCTGTCTCTGAGATGCTAAGACGGGGTGT 1500
Qy 1501 GCTTGTATGAGCTTACCGCCGCGAGACCAAGTTAGGCTTACGACATACGAAAC 1560
Db 1501 GCTTGTATGAGCTTACCGCCGCGAGACCAAGTTAGGCTTACGACATACGAAAC 1560
Qy 1561 CCGGAGCTTCCCGTGTGCAAGACATCTTGAATTTTGGAGGGGCTTTTACGGGCTC 1620
Db 1561 CCGGAGCTTCCCGTGTGCAAGACATCTTGAATTTTGGAGGGGCTTTTACGGGCTC 1620
Qy 1621 ACCGACATAGAGCCCACTTCTATCCAGACAAAGAGTGGGAAAACTTCTCTAT 1680
Db 1621 ACCGACATAGAGCCCACTTCTATCCAGACAAAGAGTGGGAAAACTTCTCTAT 1680
Qy 1681 CTGTGAGGTACCAAGCACCGTGTGCGTGAAGCTCAAGCCCTCCCGCTGTGGAC 1740
Db 1681 CTGTGAGGTACCAAGCACCGTGTGCGTGAAGCTCAAGCCCTCCCGCTGTGGAC 1740

Db 1681 CTGTGAGGTACCAAGCACCGTGTGCGTGAAGCTCAAGCCCTCCCGCTGTGGAC 1740
Qy 1741 CAGATGTGAAGTGTGTATTCGTCTCAAGCCCAACCTTCAATGGGCAACCTGTGCTA 1800
Db 1741 CAGATGTGAAGTGTGTATTCGTCTCAAGCCCAACCTTCAATGGGCAACCTGTGCTA 1800
Qy 1801 TATAGACTGGGCGCTGTCCAGAAATGAAGTCAACCTTGAAGCAACCAATGATATTC 1860
Db 1801 TATAGACTGGGCGCTGTCCAGAAATGAAGTCAACCTTGAAGCAACCAATGATATTC 1860
Qy 1861 ATGACATATATGTGGCTGACCTTGAAGGTCCTTACAGATCCTTGGGTCTGTTGGCGC 1920
Db 1861 ATGACATATATGTGGCTGACCTTGAAGGTCCTTACAGATCCTTGGGTCTGTTGGCGC 1920
Qy 1921 GTTCTGGTGTCTTGGCGGCTTATTCCTTATCCAGGCTGCTGTATGATGATAGG 1980
Db 1921 GTTCTGGTGTCTTGGCGGCTTATTCCTTATCCAGGCTGCTGTATGATGATAGG 1980
Qy 1981 ATGTCTTGTCCGGAAGCCGGCAATCATACCCGACAGGAAATCTCTACCGGAGTTT 2040
Db 1981 ATGTCTTGTCCGGAAGCCGGCAATCATACCCGACAGGAAATCTCTACCGGAGTTT 2040
Qy 2041 GATGAATGAAAGTGTCTGA 2061
Db 2041 GATGAATGAAAGTGTCTGA 2061

RESULT 6
US-09-916-359-1
; Sequence 1, Application US/09916359
; Patent No. US20020034734A1
; GENERAL INFORMATION:
; APPLICANT: Veronique Barban
; TITLE OF INVENTION: VACCINE COMPOSITION FOR PREVENTING OR
; FILE REFERENCE: PMCF97-03A
; CURRENT FILING DATE: 2001-07-26
; PRIOR FILING DATE: 1999-09-02
; PRIOR APPLICATION NUMBER: 97/02,887
; PRIOR FILING DATE: 1997-03-06
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 9379
; TYPE: DNA
; ORGANISM: Virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (320)...(9352)
; US-09-916-359-1

Query Match 86.7%; Score 1786; DB 3; Length 9379;
Best Local Similarity 91.7%; Pred. No. 0;
Matches 1888; Conservative 0; Mismatches 170; Indels 0; Gaps 0;
Qy 2 TGGGCGCTATACCGGCTTATGCGGACGACAGAGGGGCTTTGGAGTATATACCA 61
Db 3396 TGGGCGCGCATACCGGCTTATGCGGACGACAGAGGGGCTTATGAGTATATACCA 3455
Qy 62 GCTTGAACGGGCGGGGACAAAACAGGTGAGGGGTGAGTTCAAGTCTGATCAATGCGTG 121
Db 3456 GCTTGAACGGGCGGGGACAAAACAGGTGAGGGGTGAGTTCAAGTCTGATCAATGCGTG 3515
Qy 122 CCGAGACTTCTTGGCAACTGATTAACGGGCTGTGTGACTGTCTTACATGAGGCG 181
Db 3516 CCGAGACTTCTTGGCAACTGATTAACGGGCTGTGTGACTGTCTTACATGAGGCG 3575
Qy 182 GAACAGGACATTTGCGTACCTTAAGGCTCTGTTATCAAGTATACCAATGTGAC 241
Db 3576 GAACAGGACATTTGCGTACCTTAAGGCTCTGTTATCAAGTATACCAATGTGAC 3635

| | | | |
|----|------|--|------|
| QY | 242 | TAAGACCTGTAGGCGTGGCCCGCTCCCGCAAGAGGCCCGCTCATTTAAACATGACCTTGG | 301 |
| Dp | 3636 | AAGACCTTGTGGCTGGCCCGCTCCGCAAGGATGCGGTCAATGACACCTTCGACCTTGGC | 3699 |
| QY | 302 | GCTCCCTCGAACCTTTACCTGGTCAACGAAGCACGCGCATGATCTTCTGTGCGCGACGG | 361 |
| Dp | 3696 | GCTCTCGGACCTTTACCTGGTCAACGAAGCACGCCGATGTCACTTCCGTGCGCGCGGG | 3755 |
| QY | 362 | GTGATGCGAGGGGAGCGCTGCTTTCGCCCGCGCTTATCTTACTTGAAGGCTTCGG | 421 |
| Dp | 3756 | GTGATGAGGAGGGGAGCGCTGCTGTGCGCCCGGCCATTCTCTACTTGAAGGCTTCGG | 3815 |
| QY | 422 | GAGGCCCTCTGCTGTGCCCCCGACGGAACATGCGGTAGGATATTCAGAGCCCGGTATGCA | 481 |
| Dp | 3816 | GAGGCTCCCTGTGTGGCCCGCGGGGACGCGGTGGGATATTTAAGGCGCGGTGTGCA | 3879 |
| QY | 482 | CCCGTAGAGTGGCTTAAGGCGGGGACCTTATCCCGGTAGAGGCTTAAACAACATGA | 541 |
| Dp | 3876 | CCCGTAGAGTGGCTTAAGGCGGGTGAACCTTTATCCTGTGGAAGAACCTTAAGACAAACATGA | 3939 |
| QY | 542 | GGTCCCGGGTGTTCAGACAACTTCCTCCACACGACGTGCCCGACGACTAACAGTGG | 601 |
| Dp | 3936 | GGTCCCGGGTGTTCACGGAATACTCTCTCCACAGTAGTGCCCGACAGCTTCCAGGTGG | 3999 |
| QY | 602 | CCCACTTGATGCTGCCACCGGACGGTAAAGACCAAGTCCCGGCGCATACGAC | 661 |
| Dp | 3996 | CTCACCTTCATGCTCCCAACGACGGCAAAAGCACCAAGTCCCGGCTCATATGACG | 4055 |
| QY | 662 | CTCAGGGGCTAACGGGTGTGGTGCTCAACCCCTCGGTGCTGCAACATGAGGCTTTGGTG | 721 |
| Dp | 4056 | CTCACGGGCTTAAGGTGTGTAAGTACTCAACCCCTCTGTGTGCAACACTTGGGCTTTGGTG | 4115 |
| QY | 722 | CTTACATGTCCAAGGCCCATGGGATTTGATTCCTAACATCAGACATGGGTGAGCAATTA | 781 |
| Dp | 4116 | CTTACATGTCCAAGGCTCATGGGAATCGATTCCTAACATCAGACGCGGGTGAAGCAATTA | 4179 |
| QY | 782 | CTACTGCGAGCCCGATCACTGATTTCCACTACGCGCAAGTCTCTTGGCGACGGCGGGTGT | 841 |
| Dp | 4176 | CCACTGGAGGCCCATCACTGATCTCACTCAGCGCAAGTCTCTTGGCCGACGGCGGGTGTCT | 4239 |
| QY | 842 | CAGGGGGGCTTAATGACATTAATTAATTTGACGAGTGCACCTCCACGGATGCCAATATCA | 901 |
| Dp | 4236 | CGGGGGGGCTTAATGACATTAATTAATTTGACGAGTGCACCTCCACGGATGCAATATCA | 4299 |
| QY | 902 | TCTTTGGGATTTGGCACTGTCTCTTGAACGAAGAGACCGCGGGGCGAGACTGTGTC | 961 |
| Dp | 4296 | TCTTTGGGATTTGGGCACTGTCTCTTGAACGAAGAGACTGCGGGGCGAGACTGTGTGTC | 4355 |
| QY | 962 | TGCGCACCGCTAACCCCTCCGGGCTTCGTCACTGTGCCCCCATCTTAATCAACGAGAGTTG | 1021 |
| Dp | 4356 | TGCGCACCGCACCCCTCCGGGCTTCGTCACTGTGCCCCCATCTTAACGAGAGGTTG | 4415 |
| QY | 1022 | CTCTGTCACTAACCGGAGAGATCCCTTTTATGGCAAGGCTATTCCTCTTAAGAAATTA | 1081 |
| Dp | 4416 | CTCTGTCACTAACCGGAGAGATCCCTTTTATCGGGAAGGCTATTCCTCTTAAGAAATTA | 4479 |
| QY | 1082 | AGGGGGGAGACATCTCATCTTTCTTGSCACTCAAGAAAGAGTGGACGAGCTCGCGCA | 1141 |
| Dp | 4476 | AGGGGGGAGACATCTCATCTTTCTGTCAATTCAAGAAAGAGTGGACGAACTCGCGCGCA | 4539 |
| QY | 1142 | AACCTGTGCGTGGCGCTCAATGCGCGGTCTTACTACCGCGGCGCTTGATGTGTCCGTCA | 1201 |
| Dp | 4536 | AGCTGTGTGCAATTGGGCATCAATGCGCGGTCTTACTACCGCGGTCTTGATGTGTCCGTCA | 4599 |
| QY | 1202 | TCCCGACCAAGTGTACGTTGTGTGTGTGTGGCACTGACGCCCTCATTAACGGCTTTACGG | 1261 |
| Dp | 4596 | TCCCGACCAAGGGCGGATTTGTGTGTGTGTGTGGCAACGAAAGCCCTCATGACCGGCTAATACG | 4659 |
| QY | 1262 | GCGACTTGATTCGGGTATAGACTGCAACAGTGTGTCAACCGACGACGACTGTGACCTACGC | 1321 |
| Dp | 4656 | GCGACTTGACTCGGTATATAGACTGCAATAGTGTGTCAACCGACGACTGTGATTTACGC | 4715 |
| QY | 1322 | TTGACCCCTTACCTTCAACATTGAGAACATCAAGCTTCCCGAGAGTGTCTTCCGTAATC | 1381 |

| | | | |
|--|------|--|------|
| Db | 4716 | TTGACCCCTACCTTACCACTTGAAGCAATCAACGCTCCCCAGAGTCTGTCTCCGCACTC | 4775 |
| QY | 1382 | AACGTGGGGGTAGGACTTGGCAGAGGGAAGCCAGGCACTCTACAGATTGTGGCAACCGGGGG | 1441 |
| Db | 4776 | AAAGCTGGGGGAGGAGACTGGCAGGGGGGAAGCAGGCACTTACAGATTGTGGCAACCGGGGG | 4835 |
| QY | 1442 | AGCGTCTTCTGGCATGTTTGAAGCTGTGTCTCTTGGCAGTGTCTATGACGGGGGTTGTG | 1501 |
| Db | 4836 | AGCCCGCCCTCGGGCATGTTCGACTGTCCGTCTCTGTGAGTGTCTATGACGAGGCTGTG | 4895 |
| QY | 1502 | CTTGATATGAGCTTACGCCCGCCGAGACCAAGTTAGGCTATACAGCATATATGAACACC | 1561 |
| Db | 4896 | CTTGATATGAGCTTACGCCCGCCGAGACTACAGTTAGGCTATACAGCATATATGAACACC | 4955 |
| QY | 1562 | CGGAGCTTCCCGTGTGCAAGAACCATTTTAAATTTTGGAGGGGCGTCTTTACGGGCTCA | 1621 |
| Db | 4956 | CGGGGCTTCCCGTGTGCAAGAACCATTTTAAATTTTGGAGGGGCGTCTTTACGGGCTCA | 5015 |
| QY | 1622 | CCCAATATGAGCCGCCACTTCTCTATCCAGACAAAGCAGAGTGGGGAACCTTCCCTATC | 1681 |
| Db | 5016 | CTCATATATGATGCGCCACTTCTATCCAGACAAAGCAGAGTGGGGAACCTTCTCTATC | 5075 |
| QY | 1682 | TGATATGAGCTTACCAAGCCAGTGTGCGCTAGAGCTCAAGCCCTCCCGCTGCGGAGC | 1741 |
| Db | 5076 | TGATATGAGCTTACCAAGCCAGTGTGCGCTAGAGCTCAAGCCCTCCCGCTGCGGAGC | 5135 |
| QY | 1742 | AGATGTGGAAGTGTTCATCCGTCTCAAGCCCACTCTCAATGGGCAACACCTCTGTAT | 1801 |
| Db | 5136 | AGATGTGGAAGTGTTCATTCCTCAAGCCCACTCTCAATGGGCAACACCTCTGTAT | 5195 |
| QY | 1802 | ATTAGACTGGGCGCTGTCCAGATATGAGTCAACCTTGACGCAACCAAGTACCAAGTATATCA | 1861 |
| Db | 5196 | ACAGACTGGGCGCTGTTCAGATATGAGTCAACCTTGACGCAACCAAGTACCAAGTATATCA | 5255 |
| QY | 1862 | TGACATGTATGTCCGGCTGAAGCTTGAAGTGTGTCAAGATACCTGGGTCTGTTGGCGGGC | 1921 |
| Db | 5256 | TGACATGTATGTCCGGCTGAAGCTTGAAGTGTGTCAAGATACCTGGGTCTGTTGGCGGGC | 5315 |
| QY | 1922 | TTCTGGCTGCTTTGGCGCGATATGAGCTTATCCAGAGCTGCGTGTCTATGTATGTATGTAGA | 1981 |
| Db | 5316 | TTCTGGCTGCTTTGGCGCGATATGAGCTTATCCAGAGCTGCGTGTCTATGTATGTATGTAGA | 5375 |
| QY | 1982 | TTGTCTTGTCCGGAAGCCGGCAATCATATACCCGACAGGGAAGTCTCTTACCGGAGTTGC | 2041 |
| Db | 5376 | TCGTCTTGTCCGGAAGCCGGCAATCATATCTGACAGGAAGTCTCTTACCGGAGTTGC | 5435 |
| QY | 2042 | ATGAATATGGAAGATGCT 2059 | |
| Db | 5436 | ATGAATATGGAAGATGCT 5453 | |
| RESULT 7 | | | |
| US-10-445-724-1 | | | |
| / Sequence 1, Application US/10445724 | | | |
| / Publication No. US20040101829A1 | | | |
| / GENERAL INFORMATION: | | | |
| / APPLICANT: STAPLETON, JACK T. | | | |
| / APPLICANT: WUENSCHMANN, SABINA | | | |
| / TITLE OF INVENTION: A PROTEIN THAT INTERACTS WITH LIPIDS AND | | | |
| / TITLE OF INVENTION: METHODS FOR TREATING HYPERLIPIDEMIA | | | |
| / FILE REFERENCE: IOWA:045US | | | |
| / CURRENT APPLICATION NUMBER: US/10/445, 724 | | | |
| / CURRENT FILING DATE: 2003-05-27 | | | |
| / PRIOR APPLICATION NUMBER: 60/392,158 | | | |
| / PRIOR FILING DATE: 2003-05-27 | | | |
| / NUMBER OF SEQ ID NOS: 3 | | | |
| / SOFTWARE: Patentin Ver. 2.1 | | | |
| / SEQ ID NO 1 | | | |
| / LENGTH: 9401 | | | |
| / TYPE: DNA | | | |
| / ORGANISM: Hepatitis C virus | | | |
| / FEATURE: | | | |

NAME/KEY: CDS
LOCATION: (342) .. (9374)
US-10-445-724-1

Query Match 86.7%; Score 1786; DB 7; Length 9401;
Best Local Similarity 91.7%; Pred. No. 0;
Matches 1888; Conservative 0; Mismatches 170; Indels 0; Gaps 0;

QY 2 TGGGCGCTATCAAGCGCTATGCGGAGAGAGAGGCGCTTTGGAGTGCATATACCA 61
DB 3418 TGGCGCCCATCAAGCGGTAGCGCCAGAGAGAGAGGCGCTCTAGAGGTGCATATACCA 3477
QY 62 GCTTACCGCGCGGAGCAAAAACCAAGTGAAGGTGAGGTTCAGATCGTCACTGCTG 121
DB 3478 GCTTACCTGCGCGGAGCAAAAACCAAGTGAAGGTGAGGTTCAGATCGTCACTGCTG 3537
QY 122 CCCAGACTTTCCTTGGCAACCTGCAATTAACGAGGTGTGTGAGCTGTCTACATGAGCGG 181
DB 3538 CCCAAACCTTCCTGCGCAACGTGCATCAATGGGGTGTGAGCTGTCTACACGAGGCGG 3597
QY 182 GAACAAAGACCAATGCGTCACTTAAGGCTCTTATCCAGATGTAACCAATGTGAGCC 241
DB 3598 GAACAAAGACCAATGCGTCACTTAAGGCTCTTATCCAGATGTAACCAATGTGAGCC 3657
QY 242 AAGACCTGTAAGCTGAGCGCGCTCCCAAGTGCAGCTCATTAACACCATGCACTTGGG 301
DB 3658 AAGACCTGTAAGCTGAGCGCGCTCCCAAGTGCAGCTCATTAACACCATGCACTTGGG 3717
QY 302 GCTCTCGGACCTTTACCTGTGCAGAGGACGCGGATGTCATTCCTGTGCGCGAGCGG 361
DB 3718 GCTCTCGGACCTTTACCTGTGCAGAGGACGCGGATGTCATTCCTGTGCGCGAGCGG 3777
QY 352 GTGATGAGAGGAGGAGCGCTTGTGCGCGCGCTATCTTTAATTGAAGGCTCTCGG 421
DB 3778 GTGATGAGAGGAGGAGCGCTTGTGCGCGCGCTATCTTTAATTGAAGGCTCTCGG 3837
QY 422 GAGGCGCTTGTGCTGAGCGCGGAGGACATGCGGTAGGCATATTCAAGCGCGGTATGCA 481
DB 3838 GAGGCGCTTGTGCTGAGCGCGGAGGACATGCGGTAGGCATATTCAAGCGCGGTATGCA 3897
QY 482 CCGGTGAGTGGCTAAAGCGGTGACCTTGATCCCGTAGAGAGCTTTAGAGAACCATGA 541
DB 3898 CCGGTGAGTGGCTAAAGCGGTGACCTTGATCCCGTAGAGAGCTTTAGAGAACCATGA 3957
QY 542 GGTCCCCGGGTGTTCTCAAGCAACTCTCCCAACAGAGTGCCTCAAGACTACAAATG 601
DB 3958 GGTCCCCGGGTGTTCTCAAGCAACTCTCTCCACAGTATGCTCCCAAGACTTCCAGGTG 4017
QY 602 CCACCTGATGCTCCACCGGAGGAGGTAAAGAGCAAGAGTCCCGGCGGATACGAG 661
DB 4018 CCACCTGATGCTCCACCGGAGGAGGTAAAGAGCAAGAGTCCCGGCGGATACGAG 4077
QY 662 CTGAGGGCTAACAGGTGCTGATCAACCCCTCGGTGCTGCAACAAATGAGGCTTTGGT 721
DB 4078 CTGAGGGCTAACAGGTGCTGATCAACCCCTCGGTGCTGCAACAAATGAGGCTTTGGT 4137
QY 722 CTTAATGTCGAAGGCCCATGGGATTGATCTTAACATCAGAGTGGGGTGAAGCAATTA 781
DB 4138 CTTAATGTCGAAGGCCCATGGGATTGATCTTAACATCAGAGTGGGGTGAAGCAATTA 4197
QY 782 CTACTGGAGCGGATCAGGTATTCACCTAAGGAGGTTCTTGGCGAGCGGAGGTGT 841
DB 4198 CTACTGGAGCGGATCAGGTATTCACCTAAGGAGGTTCTTGGCGAGCGGAGGTGT 4257
QY 842 CAGGGGGTGTCTTATGACATTAATTTGTGAGAGTGCACCTCAAGATGCAACATCCA 901
DB 4258 CAGGGGGTGTCTTATGACATTAATTTGTGAGAGTGCACCTCAAGATGCAACATCCA 4317
QY 902 TCTTGGGAGCTTGGCACTGCTTGTGACCAAGCAAGACCGCGGGGGGAGACCTGACTGTC 961
DB 4318 TCTTGGGAGCTTGGCACTGCTTGTGACCAAGCAAGACCGCGGGGGGAGACCTGACTGTC 4377
QY 962 TCGCCACGCTACCCCTCGGGGCTCGGTCACTGTGCCCATCTTAACATGAGAGGTGG 1021

DB 4378 TCGCCACGCGCACCCCTCGGGCTCGTCACTGTGCCCATCCAAATCGAGAGGTGG 4437
QY 1022 CTCTGTCCATACCGGAGAGATCCCTTTTATGGAAGCTATTCCTCTGAAGCAATTA 1081
DB 4438 CTCTGTCCATACCGGAGAGATCCCTTTTATGGAAGCTATTCCTCTGAAGCAATTA 4497
QY 1082 AGGGGGGAGACATCTCTCTGCACTCAAAAGAAAGTGCAGAGCTCGCGGCA 1141
DB 4498 AGGGGGGAGACATCTCTCTGCACTCAAAAGAAAGTGCAGAGCTCGCGGCA 4557
QY 1142 AACTGTGCGGTGGGCGTCAATGCGGTGCTTACTACCGGCGCTTGAATGTGCTGCA 1201
DB 4558 AACTGTGCGGTGGGCGTCAATGCGGTGCTTACTACCGGCGCTTGAATGTGCTGCA 4617
QY 1202 TCCGACCAAGTGTACCTGTGCTGCTGAGCACTGAGCGCTCATGACCGGCTTACG 1261
DB 4618 TCCGACCAAGTGTACCTGTGCTGCTGAGCACTGAGCGCTCATGACCGGCTTACG 4677
QY 1262 GCGACTTGATTCGGGTATGACTGCAACAGTGTGCAACCGAGAGTGCATTCAGCC 1321
DB 4678 GCGACTTGATTCGGGTATGACTGCAACAGTGTGCAACCGAGAGTGCATTCAGCC 4737
QY 1322 TTGACCTTACCTTCACTTGAACAATCAAGCTTCCCAAGATGCTGTCTCCGTAATC 1381
DB 4738 TTGACCTTACCTTCACTTGAACAATCAAGCTTCCCAAGATGCTGTCTCCGTAATC 4797
QY 1382 AAGCTCGGGGTAGACTGAGCAGAGGAAAGCAAGGACTTACAGATTTGTGTGACCGGGG 1441
DB 4798 AAGCTCGGGGTAGACTGAGCAGAGGAAAGCAAGGACTTACAGATTTGTGTGACCGGGG 4857
QY 1442 AGCGTCTTCTGGGACATGTTTGAATGCTGTGCTCTGAGAGTGTATGACGCGGGTGTG 1501
DB 4858 AGCGTCTTCTGGGACATGTTTGAATGCTGTGCTCTGAGAGTGTATGACGCGGGTGTG 4917
QY 1502 CTGTGATGAGCTTACGCGCGCGGAGACCAAGTTAGGCTACGAGCATACATGAACCC 1561
DB 4918 CTGTGATGAGCTTACGCGCGCGGAGACCAAGTTAGGCTACGAGCATACATGAACCC 4977
QY 1562 CGGACCTTCCGCTGTGCAAGCAACATCTTGAATTTTGGAGAGGCGCTTTACGGGTCTCA 1621
DB 4978 CGGACCTTCCGCTGTGCAAGCAACATCTTGAATTTTGGAGAGGCGCTTTTACGGGTCTCA 5037
QY 1622 CCCACATGAGCGCCACTTCCATCCAGACCAAGAGAGTGGGAAAACTTCCCTATTC 1681
DB 5038 CCCACATGAGCGCCACTTCCATCCAGACCAAGAGAGTGGGAAAACTTCCCTATTC 5097
QY 1682 TGGTACGTAACCAACCAACCGGTGCGGTAGAGCTCAAGCCCTCCCGTGTGGAGC 1741
DB 5098 TGGTACGTAACCAACCAACCGGTGCGGTAGAGCTCAAGCCCTCCCGTGTGGAGC 5157
QY 1742 AGATGTGAAGTCTTGAATTCGTCTCAAGGCCCACTCTCAATGAGGCAACCTCTGCTAT 1801
DB 5158 AGATGTGAAGTCTTGAATTCGTCTCAAGGCCCACTCTCAATGAGGCAACCTCTGCTAT 5217
QY 1802 ATAGAATGGGCGCTGTCAGAAATGAAGTCAACCTAGCAACCAAGTCAACAGTATATCA 1861
DB 5218 ATAGAATGGGCGCTGTCAGAAATGAAGTCAACCTAGCAACCAAGTCAACAGTATATCA 5277
QY 1862 TGAATGTATGTCGCTGACTGAGAGTCTGTCACAGATACCTGGGTGCTGTTGCGGG 1921
DB 5278 TGAATGTATGTCGCTGACTGAGAGTCTGTCACAGATACCTGGGTGCTGTTGCGGG 5337
QY 1922 TTCTGGCTGCTTTGGCGCGGTATTTGCTATCAACAGGCTGCTGTATAGTGAAGTAAGA 1981
DB 5338 TTCTGGCTGCTTTGGCGCGGTATTTGCTATCAACAGGCTGCTGTATAGTGAAGTAAGA 5397
QY 1982 TTGTCTGTGCGGGAAGCGGCAATCATACCGGACAGGGAAGTCTCTTACCGGAGTTCG 2041
DB 5398 TTGTCTGTGCGGGAAGCGGCAATCATACCGGACAGGGAAGTCTCTTACCGGAGTTCG 5457
QY 2042 ATGAATGGAAGAGTGTCT 2059

Db 5458 ATGAGATGAGAGTGTCT 5475

RESULT 8
US-09-881-239-2
; Sequence 2, Application US/09881239
; Publication No. US20020192639A1
; GENERAL INFORMATION:
; APPLICANT: CHIEN, David Y
; APPLICANT: ARCHANGE, Phillip
; APPLICANT: TANDESK, Laura
; APPLICANT: GEORGE-NASCIMENTO, Carlos
; APPLICANT: COIT, Doris
; APPLICANT: MEDINA-SELBY, Angelica
; TITLE OF INVENTION: KEY ANTIGEN/ANTIBODY COMBINATION ASSAY
; FILE REFERENCE: 2302-16073 / P16073.003
; CURRENT APPLICATION NUMBER: US/09/881,239
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 2058
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; NAME/KEY: CDS
; LOCATION: (1)..(2058)
US-09-881-239-2

Query Match 86.4%; Score 1781.2; DB 3; Length 2058;
Beet Local Similarity 91.6%; Pred. No. 0; Mismatches 173; Indels 0; Gaps 0;
Matches 1885; Conservative 0;

Qy 1 ATGGCGCTTATCAGCGCTTATGCCCCAGACAGAGAGGCGCTTTTGGAGATGATAATCAC 60
Db 1 ATGGCGCCCATACAGCGCGTATAGCCCCAGACAGAGAGGCGCTTCTAGGGTGCATATATCAC 60

Qy 61 AGCTTGACCGGCGCGGAGCAAAAACAGGTGAGGTGAGGTTCAGATCTGTCTCAACTGCT 120
Db 61 AGCTTATCTGCGCGGAGCAAAAACAGGTGAGGTGAGGTTCAGATCTGTCTCAACTGCT 120

Qy 121 GCCCAGACTTCTTGGCAACCTGCAATTAAGGGGTGTGTGGACTGTCAACCATGAGAGC 180
Db 121 GCCCAAACTTCTTGGCAACCTGCAATTAAGGGGTGTGTGGACTGTCTTCAACCGAGCC 180

Qy 121 GCGCAGACTTCTTGGCAACCTGCAATTAAGGGGTGTGTGGACTGTCAACCATGAGAGC 180
Db 121 GCGCAGACTTCTTGGCAACCTGCAATTAAGGGGTGTGTGGACTGTCTTCAACCGAGCC 180

Qy 181 GGAACAGAGACCATTTGCGTCACTTAAGGGTCTCTTATTCAGATGTACCAATGTGAGC 240
Db 181 GGAACAGAGACCATTTGCGTCACTTAAGGGTCTCTTATTCAGATGTATCAATGTGAGC 240

Qy 241 CAAGACCTGTGAGGTGCGTCCGCTCCCAAGGTGCCCTCTTAAACACATGACCTTGC 300
Db 241 CAAGACCTGTGAGGTGCGTCCGCTCCCAAGGTGCCCTCTTAAACACATGACCTTGC 300

Qy 241 CAAGACCTGTGAGGTGCGTCCGCTCCCAAGGTGCCCTCTTAAACACATGACCTTGC 300
Db 241 CAAGACCTGTGAGGTGCGTCCGCTCCCAAGGTGCCCTCTTAAACACATGACCTTGC 300

Qy 301 GGCCTCTGAGACCTTAACTGTGACAGAGGACGCGGATGATTCCTGTGGCGGAGAG 360
Db 301 GGCCTCTGAGACCTTAACTGTGACAGAGGACGCGGATGATTCCTGTGGCGGAGAG 360

Qy 361 GGTGATGAGGAGGAGCGCTGTCTTTCGCCCCGCGCTATCTCTTAAAGAGCTCTCG 420
Db 361 GGTGATGAGGAGGAGCGCTGTCTTTCGCCCCGCGCTATCTCTTAAAGAGCTCTCG 420

Qy 421 GAGAGCGCTCTGTCTGTGCCCCGAGAGACATGCGGTGAGGATTTTGAAGCGCGGTATGC 480
Db 421 GAGAGCGCTCTGTCTGTGCCCCGAGAGACATGCGGTGAGGATTTTGAAGCGCGGTATGC 480

Qy 481 ACCCGTGAAGGTCTTAAGCGGAGGATTCATCCCGTGAAGAGGCTTGAAGCAACATG 540
Db 481 ACCCGTGAAGGTCTTAAGCGGAGGATTCATCCCGTGAAGAGGCTTGAAGCAACATG 540

Qy 541 AGGTCCCGGAGTGTCTCAAGACAACTCTCCAGCAGCAGTGCCTCCAGAGCTTACCAAGTG 600
Db 541 AGGTCCCGGAGTGTCTCAAGACAACTCTCTCCAGCAGTGTGCCAGAGCTTCCAGGTG 600

Db 541 AGGTCCCGGAGTGTCTCAAGACAACTCTCTCCAGCAGTGTGCCAGAGCTTCCAGGTG 600
Qy 601 GCCCACTGTGATGCTCTCCACCGGAGCGGTAAAGACCAAGGTCTCCGCGCATATACCA 660
Db 601 GCTCACTTCATGCTCTCCACAGGAGCGGCAAAAGACCAAGGTCTCCGCGCATATATCA 660

Qy 661 GCTCAAGGCTCAAGAGTGTGTGCTCAACCCCTCCGTGCTGCAACAATGGGCTTTGGT 720
Db 661 GCTCAAGGCTCAAGAGTGTGTGCTCAACCCCTCCGTGCTGCTGCAACAATGGGCTTTGGT 720

Qy 721 GCTTACATGTCGAAGGCCCATGAGATTGATCTTAAATCAGAGACTGGGGTGAACAATT 780
Db 721 GCTTACATGTCGAAGGCCCATGAGATTGATCTTAAATCAGAGACTGGGGTGAACAATT 780

Qy 781 ACTACTGGACCGCGATACGTAATTCACCTTAACGCGCAAGTTCTTGGCCGAGCGGGTGT 840
Db 781 ACCACTGGACCGCGCATACGTAATTCACCTTAACGCGCAAGTTCTTGGCCGAGCGGGTGT 840

Qy 841 TCAGGGGTGCTTATGACATATATAATTGTGACAGAGTCCCACTCCAGGATGCAATCC 900
Db 841 TCAGGGGTGCTTATGACATATATAATTGTGACAGAGTCCCACTCCAGGATGCAATCC 900

Qy 901 ATCTTGGCATTTGACATGCTCTTGAACAGACAGACCGCGGGGCGAGACTGTG 960
Db 901 ATCTTGGCATTTGACATGCTCTTGAACAGACAGACCGCGGGGCGAGACTGTG 960

Qy 961 CTGCGCAACCGCTACCCCTCCGGGCTCCGCTCACTGCCCCCACTCTTAATGAGAGGTT 1020
Db 961 CTGCGCAACCGCTACCCCTCCGGGCTCCGCTCACTGCCCCCACTCTTAATGAGAGGTT 1020

Qy 1021 GCTCTGTCACTACCGAGAGATCCCTTTATGCGCAAGGCTATCCCTTGAACAAATT 1080
Db 1021 GCTCTGTCACTACCGAGAGATCCCTTTATGCGCAAGGCTATCCCTTGAACAAATT 1080

Qy 1081 AAGGGGGGAGACATCTCATCTTCTGCACTAAAGAAAGTGCAGAGCTGCCGCA 1140
Db 1081 AAGGGGGGAGACATCTCATCTTCTGCACTAAAGAAAGTGCAGAGCTGCCGCA 1140

Qy 1141 AAACGTGTGTGAGGTGAGTCAATGCGGTCTTAATCCCGGCTTGAATGTGCGCTG 1200
Db 1141 AAACGTGTGTGAGGTGAGTCAATGCGGTCTTAATCCCGGCTTGAATGTGCGCTG 1200

Qy 1201 ATCCGACCAATGAGAGCTTGTGCTGCTGCAACTGACGCGCTCATGACCGGCTTTATC 1260
Db 1201 ATCCGACCAATGAGAGCTTGTGCTGCTGCAACTGACGCGCTCATGACCGGCTTTATC 1260

Qy 1261 GCGCATCTTGAATGCGGTATGACTGCAACAGTGTGACCCAGACAGTGCATTTCAAC 1320
Db 1261 GCGCATCTTGAATGCGGTATGACTGCAACAGTGTGACCCAGACAGTGCATTTCAAC 1320

Qy 1321 CTGACCCCTACCTTCACTGAGACATCAACGCTTCCCGAGAGTGTCTCCGCTACT 1380
Db 1321 CTGACCCCTACCTTCACTGAGACATCAACGCTTCCCGAGAGTGTCTCCGCTACT 1380

Qy 1381 CAACGTGCGGGTAAAGACTGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1440
Db 1381 CAACGTGCGGGTAAAGACTGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1440

Qy 1441 GAGCGTCTTGTGAGATTTTGAATGCTGTGTCTCTGCGAGTGTGATGAGCGGGTGT 1500
Db 1441 GAGCGTCTTGTGAGATTTTGAATGCTGTGTCTCTGCGAGTGTGATGAGCGGGTGT 1500

Qy 1501 GCTTGTGATGAGCTTAAAGCGCGCGAGACCAAGTGAAGCTTAAAGCTTAAAGCAAC 1560
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Qy 1681 CTGGTAGGCTACCAAGCCAGCTGCGCTAGAGCTCAAGCCCTCCCGCGTGGAGC 1740
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Db 1741 CAGATGTGGAGTGTGATCCGTCTCAAGCCACCTTCATGGGCAACCTCTGTCTA 1800
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Db 1801 TACACACTGGGCGCTGTCCAGAAATGAAGTCAACCTTCAGGACCCAGTCAACCAAGTATTC 1860
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Qy 1921 GTTCTGCTGTCTTTGGCCGCGTATTCCTATCCAGAGCTGCGTGTCAATAGTATAG 1980
Db 1921 GTTCTGCTGTCTTTGGCCGCGTATTCCTATCCAGAGCTGCGTGTCAATAGTATAG 1980
Qy 1981 ATTGCTTGTCTCGGAAAGCCGCGCATCATCCCGACAGGAAAGTCTCTACCGGAGTTC 2040
Db 1981 GTGCTGTGTCTCGGAAAGCCGCGCATCATCTGACAGGAAAGTCTCTACCGAGTTC 2040
Qy 2041 GATGAATGGAAGAGTGC 2058
Db 2041 GATGAATGGAAGAGTGC 2058

RESULT 9

US-10-643-853-2
; Sequence 2, Application US/10643853
; Publication No. US20040098622A1
; GENERAL INFORMATION:
; APPLICANT: CHIEN, David Y.
; APPLICANT: ARCANDEL, Phillip
; APPLICANT: TANDESK, Laura
; APPLICANT: GEORGE-NASCIMENTO, Carlos
; APPLICANT: COIT, Doris
; APPLICANT: MEDINA-SELBY, Angelica
; TITLE OF INVENTION: HCV ANTIGEN/ANTIBODY COMBINATION ASSAY
; FILE REFERENCE: 2302-16073 / P16073.003
; CURRENT APPLICATION NUMBER: US/10/643,853
; PRIOR FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: US/09/881,239
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 2058
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: representative NS3/4a conformational antigen
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2058)
US-10-643-853-2

Query Match 86.4%; Score 1781.2; DB 7; Length 2058;
Best Local Similarity 91.6%; Pred. No. 0;
Matches 1885; Conservative 0; Mismatches 173; Indels 0; Gaps 0;
Qy 1 ATGGGCGCTATCAGGCGCTATGCTCCAGACAGAGAGGCGCTTTGGAGTCAATATCAC 60
Db 1 ATGGGCGCTATCAGGCGCTATGCTCCAGACAGAGAGGCGCTTTGGAGTCAATATCAC 60
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Qy 181 GGAACAGAGACATTTGCTGACCTTAAGGCTCTGTATTCAGATGTATACCAATGTGAC 240
Db 181 GGAACAGAGACATTTGCTGACCTTAAGGCTCTGTATTCAGATGTATTAACCAATGTGAC 240
Qy 241 CAAGACTGTAGGCTGGCCGCTCCCAAGGTGCGGCTCATTAACACCAATGACTTGC 300
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Db 361 GGTATGACAGGGGAGCTGTCTGTGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
Qy 421 GGAAGCCCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
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Qy 2041 GATGAATGGAAGATGC 2058
Db 2041 GATGAATGGAAGATGC 2058
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RESULT 10
US-10-658-782-1

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; Sequence 1, Application US/10658782
; Publication No. US20040142321A1
; GENERAL INFORMATION:
; APPLICANT: ARCANDEL, Phillip
; APPLICANT: CHIEN, David Y.
; TITLE OF INVENTION: HCV ASSAY
; FILE REFERENCE: 2300-19199
; CURRENT APPLICATION NUMBER: US/10/658,782
; CURRENT FILING DATE: 2003-09-08
; PRIOR APPLICATION NUMBER: 60/409,515
; PRIOR FILING DATE: 2002-09-09
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; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 1
; LENGTH: 2058
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: NS3/41 conformational epitope DNA sequence
US-10-658-782-1
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Query Match 86.4%; Score 1781.2; DB 7; Length 2058;
Beet Local Similarity 91.6%; Pred. No. 0;
Matches 1885; Conservative 0; Mismatches 173; Indels 0; Gaps 0;
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Qy 1 ATGGGCGCTATCAGGCTTATGCCAGACGACAGGGGCTTTGGAGTGCATATATCAC 60
Db 1 ATGGGCGCTATCAGGCTTATGCCAGACGACAGGGGCTTTGGAGTGCATATATCAC 60
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DB 1081 AAGGGGGGAGACATCTCATCTTTCGCCACTCAAGAAAGAGTGCAGAGACTCGCCCA 1140
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QY 1921 GTTGT 1980
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QY 1981 ATGT 2040
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QY 2041 GATGAAATGAAAGTGTG 2058
DB 2041 GATGAAATGAAAGTGTG 2058

RESULT 11
US-09-881-654-1
; Sequence 1, Application US/09881654
; Patent No. US2002014685A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, David Y.
; APPLICANT: ARANGEL, Phillip
; APPLICANT: TANDESKIE, Laura
; APPLICANT: GEORGE-NASCIENTE, Carlos
; APPLICANT: COLT, Doris
; APPLICANT: MEDINA-SELBY, Angelica
; TITLE OF INVENTION: IMMUNOSAYS FOR ANTI-HCV ANTIBODIES
; FILE REFERENCE: 2302-17039 / P17039.002
; CURRENT APPLICATION NUMBER: US/09/881,654
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 60/212,082
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/280,811
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 60/280,867
; PRIOR FILING DATE: 2001-04-02
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO: 1
; LENGTH: 2058
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: representative NS3/4a conformational antigen
; NAME/KEY: CDS
; LOCATION: (1) .. (2058)
; US-09-881-654-1

Query Match 86.3%; Score 1779.6; DB 3; Length 2058;
Best Local Similarity 91.5%; Pred. No. 0; Mismatches 174; Indels 0; Gaps 0;
Matches 1884; Conservative 0; Mismatches 174; Indels 0; Gaps 0;

QY 1 ATGGGCGCTATCACGGCTATGCTCCAGCAGACAAAGGGCTTTTGGATGATATATCAC 60
DB 1 ATGGGCGCTATCACGGCTATGCTCCAGCAGACAAAGGGCTTTTGGATGATATATCAC 60
QY 61 AGCTTACCGCGCGGGGACAAACCAAGGTGAGGTGAGTTCAGATGTGTCAACTGCT 120
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Db 1441 GAGCGCGCTCTGAGATGTTGACTGCTGCTCTGCGAGTGTATGACCGGGATTT 1500

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RESULT 12
US-10-637-323-1
; Sequence 1, Application US/10637323
; Publication No. US20040063092A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, David Y.
; APPLICANT: ARANGEL, Phillip
; APPLICANT: TANDESK, Laura
; APPLICANT: GEORGE-MASCIMENTO, Carlos
; APPLICANT: COLT, Doris
; APPLICANT: MEDINA-SELBY, Angelica
; TITLE OF INVENTION: IMMUNOSAYS FOR ANTI-HCV ANTIBODIES
; FILE REFERENCE: 2302-17039 / P/17039.002
; CURRENT APPLICATION NUMBER: US/10/637,323
; CURRENT FILING DATE: 2003-08-08
; PRIOR APPLICATION NUMBER: US/09/881,654
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 60/212,082
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/280,811
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 60/280,867
; PRIOR FILING DATE: 2001-04-02
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2058
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:

OTHER INFORMATION: representative NS3/4a conformational antigen
FEATURE:
NAME/KEY: CDS
LOCATION: (1).. (2058)
US-10-637-323-1

Query Match 86.3%; Score 1779.6; DB 7; Length 2058;
Best Local Similarity 91.5%; Pred. No. 0;
Matches 1884; Conservative 0; Mismatches 174; Indels 0; Gaps 0;

QY 1 ATGGGCGCTATACGCGCTATATGCGAGAGAGGCGCTTTGGATGATATACAC 60
DB 1 ATGGGCGCTATACGCGCTATATGCGAGAGAGGCGCTTTGGATGATATACAC 60
QY 61 AGCTTGACCGGCGGAGCAAAAACAGGTGAGGGTGAAGTTCAGATGTCATCTGT 120
DB 61 AGCTTGACCGGCGGAGCAAAAACAGGTGAGGGTGAAGTTCAGATGTCATCTGT 120
QY 121 GCCGACCTTTCTTGGCAACCTGCAATTAAGGGGTGTGTGGACTGTCTACATGAGCC 180
DB 121 GCCGACCTTTCTTGGCAACCTGCAATTAAGGGGTGTGTGGACTGTCTACATGAGCC 180
QY 181 GGAACAGAGACCATGCGCTACCTAAGGCTCTGTATCCAGATGTAACCAATGTGAC 240
DB 181 GGAACAGAGACCATGCGCTACCTAAGGCTCTGTATCCAGATGTAATCAATGTGAC 240
QY 241 CAAGACCTTGTAGGCTGCGCGCTCCCAAGGTGCGCTATTAACACATGCACTTGC 300
DB 241 CAAGACCTTGTAGGCTGCGCGCTCCCAAGGTGCGCTATTAACACATGCACTTGC 300
QY 301 GGCCTCGGAGCTTTACCTGTCACAGAGGACGCGGATGTCATTCCTGTGCGGAGCG 360
DB 301 GGCCTCGGAGCTTTACCTGTCACAGAGGACGCGGATGTCATTCCTGTGCGGAGCG 360
QY 361 GGTGAATGAGAGGGAGCGCTGCTGTGCGCGGCGCATTTCTTAAAGAGCTCTGCG 420
DB 361 GGTGAATGAGAGGGAGCGCTGCTGTGCGCGGCGCATTTCTTAAAGAGCTCTGCG 420
QY 421 GGAAGCCCTCTGTGTGCGCGGAGCAATGCGGTAGGCAATTCAGAGCGCGGTATGC 480
DB 421 GGAAGCCCTCTGTGTGCGCGGAGCAATGCGGTAGGCAATTCAGAGCGCGGTATGC 480
QY 481 ACCCGTAGAGTGAAGCGGTGAGCTTATCCCGTAGAGAGCTTAGAGCAACATG 540
DB 481 ACCCGTAGAGTGAAGCGGTGAGCTTATCCCGTAGAGAGCTTAGAGCAACATG 540
QY 541 AGGTCCCGGTGTTCACGGAATACCTCTCTCCACAGATGTGCCAGAGCTTCCAGGTG 600
DB 541 AGGTCCCGGTGTTCACGGAATACCTCTCTCCACAGATGTGCCAGAGCTTCCAGGTG 600
QY 601 GCCGACCTGATGCTCCACCGGAGCGGTAAAGAGCAAGAGTCCCGCGCATACGCA 660
DB 601 GCCGACCTGATGCTCCACCGGAGCGGTAAAGAGCAAGAGTCCCGCGCATACGCA 660
QY 661 GGTCAAGGCTAAGAGTGTGAGTCAACCCCTCGTTGTCGCAACATAGGGCTTTGGT 720
DB 661 GGTCAAGGCTAAGAGTGTGAGTCAACCCCTCGTTGTCGCAACATAGGGCTTTGGT 720
QY 721 GCTTACATGTCCAGAGCCCATGATTTATCTTAAATCAGAGATGAGGATGAGCAAT 780
DB 721 GCTTACATGTCCAGAGCCCATGATTTATCTTAAATCAGAGATGAGGATGAGCAAT 780
QY 781 ACTTACTGAGAGCCCATGATTTATCTTAAATCAGAGATGAGGATGAGCAAT 840
DB 781 ACTTACTGAGAGCCCATGATTTATCTTAAATCAGAGATGAGGATGAGCAAT 840
QY 841 TCAGAGGAGGCTTATGAGCAATTAATTTGTGAGAGTGCATCCACGAGTGCATCC 900
DB 841 TCAGAGGAGGCTTATGAGCAATTAATTTGTGAGAGTGCATCCACGAGTGCATCC 900
QY 901 ATCTTGGGCAATTTGCACTGTCTTGAACAGAGAGAGCGCGGGGCGAGATGACTGTG 960
DB 901 ATCTTGGGCAATTTGCACTGTCTTGAACAGAGAGAGCGCGGGGCGAGATGACTGTG 960

QY 961 CTGCGCACCGGTACCCCTCCGGGCTCGGTACTGTGACCCCATCTAATCATGAGAGGT 1020
DB 961 CTGCGCACCGGTACCCCTCCGGGCTCGGTACTGTGACCCCATCTAATCATGAGAGGT 1020
QY 1021 GCTCTGTCCACTACCGAGAGATCCCTTTTATGAGCAAGCTATTCCTCTTGAACAT 1080
DB 1021 GCTCTGTCCACTACCGAGAGATCCCTTTTATGAGCAAGCTATTCCTCTTGAACAT 1080
QY 1081 AAGGGGGAGACATCTCATCTTGTGCACTCAAGAAAGAGTGTGAGAGTGTGCGGCA 1140
DB 1081 AAGGGGGAGACATCTCATCTTGTGCACTCAAGAAAGAGTGTGAGAGTGTGCGGCA 1140
QY 1141 AAAGTGTGCGGTTGGGGGTCAATGCGGTGCTTACTGCGGCGCTTATGTGCGGTC 1200
DB 1141 AAAGTGTGCGGTTGGGGGTCAATGCGGTGCTTACTGCGGCGCTTATGTGCGGTC 1200
QY 1201 ATCCGACCAAGTGTGAGCTTGTGCTGTGCAACCTGACGCGCTCATGACCGGCTTAA 1260
DB 1201 ATCCGACCAAGTGTGAGCTTGTGCTGTGCAACCTGACGCGCTCATGACCGGCTTAA 1260
QY 1261 GCGGACTTGTGATGCTGTGATGAGCTGCAACAGTGTGACCCAGACAGTGTGACG 1320
DB 1261 GCGGACTTGTGATGCTGTGATGAGCTGCAACAGTGTGACCCAGACAGTGTGACG 1320
QY 1321 CTGACCCCTACCTTACCATTTGAGCAATTCAGATGCTTCCCGAGAGTGTGCGGTA 1380
DB 1321 CTGACCCCTACCTTACCATTTGAGCAATTCAGATGCTTCCCGAGAGTGTGCGGTA 1380
QY 1381 CAACGTCGGGGTGTGAGCTGTGAGAGAGGAGGAGGAGCATCTACAGATTTGTGCA 1440
DB 1381 CAACGTCGGGGTGTGAGCTGTGAGAGAGGAGGAGGAGCATCTACAGATTTGTGCA 1440
QY 1441 GAGCGTCTTCTGTGAGTGTGATCTGTGTGTCTGTGAGTGTGATGAGCGGCTGT 1500
DB 1441 GAGCGTCTTCTGTGAGTGTGATCTGTGTGTCTGTGAGTGTGATGAGCGGCTGT 1500
QY 1501 GGTGTGTGAGCTTACGCGCGGAGCAACAGTGTGAGCTTACGAGCAATGAAAC 1560
DB 1501 GGTGTGTGAGCTTACGCGCGGAGCAACAGTGTGAGCTTACGAGCAATGAAAC 1560
QY 1561 CCGGACTTCCCGTGTGCAAGACCATCTTGAATTTGGAGGGCGCTTTACGGGTCT 1620
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QY 1621 ACCCATAGACGCGCTTCTTATCCAGACAAAGAGAGTGGGAAAACCTTCTTAT 1680
DB 1621 ACCCATAGACGCGCTTCTTATCCAGACAAAGAGAGTGGGAAAACCTTCTTAT 1680
QY 1681 CTGTGAGGTACCAAGCCAGCGGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1740
DB 1681 CTGTGAGGTACCAAGCCAGCGGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1740
QY 1741 CAGATGTGAGTGTGATCTGATCTCAAGCCCATCTTCAATGAGGCAACCTTGTCT 1800
DB 1741 CAGATGTGAGTGTGATCTGATCTCAAGCCCATCTTCAATGAGGCAACCTTGTCT 1800
QY 1801 TATAGACTGGGCGCTGTCAAGATGAGTCAACCTTGAAGCAACCAATGATATC 1860
DB 1801 TATAGACTGGGCGCTGTCAAGATGAGTCAACCTTGAAGCAACCAATGATATC 1860
QY 1861 ATGAGATGATGTGCGGTGAGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1920
DB 1861 ATGAGATGATGTGCGGTGAGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1920
QY 1921 GTTCTGAGCTTGTGGCGGCTATGCTTATCAAGAGTGTGAGTGTGAGTGTGAGT 1980
DB 1921 GTTCTGAGCTTGTGGCGGCTATGCTTATCAAGAGTGTGAGTGTGAGTGTGAGT 1980
QY 1981 ATTTGCTTGTCCGAAAGCCCGCAATCATACCCGACAGGAAAGTCTTACCGGAGTTC 2040
DB 1981 ATTTGCTTGTCCGAAAGCCCGCAATCATACCCGACAGGAAAGTCTTACCGGAGTTC 2040

QY 2041 GATGAATGAGAGTGC 2058
Db 2041 GATGAGATGAGAGTGC 2058

RESULT 13
US-10-899-715-1
; Sequence 1, Application US/10899715
; Publication No. US20040265801A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, David Y.
; APPLICANT: ARANGEL, Phillip
; APPLICANT: TANDESKE, Laura
; APPLICANT: GEORGE-NASCIMENTO, Carlos
; APPLICANT: COLT, Doris
; APPLICANT: MEDINA-SELBY, Angelica
; TITLE OF INVENTION: IMMUNOSSAYS FOR ANTI-HCV ANTIBODIES
; FILE REFERENCE: 2302-17039 / P17039.002
; CURRENT APPLICATION NUMBER: US/10/899,715
; CURRENT FILING DATE: 2004-07-26
; PRIOR APPLICATION NUMBER: US/09/881,654
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 60/212,082
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/280,811
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 60/280,867
; PRIOR FILING DATE: 2001-04-02
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2058
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Representative NS3/4a conformational antigen
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2058)
; US-10-899-715-1

Query Match 86.3%; Score 1779.6; DB 8; Length 2058;
Best Local Similarity 91.5%; Pred. No. 0;
Matches 1884; Conservative 0; Mismatches 174; Indels 0; Gaps 0;

QY 1 ATGGGCGCTATCAAGCGCTATATGCCAGACAGACAGAGGCGCTTTGGGATGATATCAC 60
Db 1 ATGGGCGCCCATACGGCGCTATACGCCAGACAGAGGCGCTCTAGGGTGATATATCAC 60

QY 61 AGCTTGACCGCGCGGGGACAAAACAGGTGGAGGGGTTCAGATGTGTCACTGCT 120
Db 61 AGCTTAACGTGGCGGGACAAAACAGGTGGAGGGGTTCAGATGTGTCACTGCT 120

QY 121 GCCCAGACTTTCTTGCACTGCAATTAACGGGAGTGTGGACTGTACCATGAGAC 180
Db 121 GCCCAACCTTCTTGCACTGCAATTAACGGGAGTGTGTGAGACTGTACCATGAGAC 180

QY 181 GGAACAGAGACATTTGCTACCTTAAGGCTCTGTTATCCAGATGTACCAATGTGAC 240
Db 181 GGAACAGAGACATTTGCTACCTTAAGGCTCTGTTATCCAGATGTATCCAAATGTAGAC 240

QY 241 CAAGACCTGTAGGCTGGCGGCTCCCAAGGTGCGCGCTCATTAACCAACGACCTTGC 300
Db 241 CAAGACCTGTAGGCTGGCGGCTCCCAAGGTGCGCGCTCATTAACCAACCTTGC 300

QY 301 GGCTCTCGGACCTTTACTGTGTCAAGAGCACGGCGATGATCTTCTGTGCGCGAGCG 360
Db 301 GGCTCTCGGACCTTTACTGTGTCAAGAGCACGGCGATGATCTTCTGTGCGCGAGCG 360

QY 361 GGATGAGGAGGAGCGCTGCTTTGCGCCCGGCTTATCTTTACTTTGAAAGGCTCTCG 420
Db 361 GGATGAGGAGGAGCGCTGCTTTGCGCCCGGCTTATCTTTACTTTGAAAGGCTCTCG 420

QY 421 GAGGCGCTTGTGTGCCCCCGACAGACATGCGGAGGATATTGAGAGCGCGGATGC 480
Db 421 GAGGCGCTTGTGTGCCCCCGAGGACAGCGGATATTGAGAGCGCGGATGC 480

QY 481 ACCGCTGAGATGTCTTAAGCGGCTGATCTTCAATCCCGTGAAGAGCTTAAGACAACTAG 540
Db 481 ACCGCTGAGATGTCTTAAGCGGCTGATCTTCAATCCCGTGAAGAGCTTAAGACAACTAG 540

QY 541 AGGTCCCGGCTTCTCAAGACATCTCTCCCAACAGAGTGCACCAAGCTTCAAGAGT 600
Db 541 AGGTCCCGGCTTCTCAAGAGATCTCTCTCAACAGAGTGCACCAAGCTTCAAGAGT 600

QY 601 GCCCACTGATGCTCCACAGGCGGATTAAGACACCAAGTCCCGGCGCATATACGA 660
Db 601 GCTCACTTCACTGCTCCACAGGCGGATTAAGACACCAAGTCCCGGCTGATATGCA 660

QY 661 GCTCAGGCTTCAAGAGTGTGTCTCAACCTCTCGTGTGCAACAATGGGCTTTGAT 720
Db 661 GCTCAGGCTTCAAGAGTGTGTCTCAACCTCTGTGTGCAACAATGGGCTTTGAT 720

QY 721 GCTTACATGTCCAAAGGCGCATGAGATTTATCTTAATCAGAGCTGGGCTGAGCAATT 780
Db 721 GCTTACATGTCCAAAGGCTCATGAGATTTATCTTAATCAGAGCTGGGCTGAGCAATT 780

QY 781 ACTACTGGCAGCGCGATGACGATTCACCTTACCGGCAAGTTCTTGGCCGACGGGCTGT 840
Db 781 ACTACTGGCAGCGCGATGACGATTCACCTTACCGGCAAGTTCTTGGCCGACGGGCTGT 840

QY 841 TCAGGGGCTGTATGACATATATATTTGTGACAGAGTCCACTCCAGGATGCCATGCC 900
Db 841 TCAGGGGCTGTATGACATATATATTTGTGACAGAGTCCACTCCAGGATGCCATGCC 900

QY 901 ATCTTGGGATTTGGACATGTCTTGAACCAAGACAGACCGGGGGCCGAGCTGACTGTG 960
Db 901 ATCTTGGGATTTGGACATGTCTTGAACCAAGACAGACCGGGGGCCGAGCTGACTGTG 960

QY 961 CTCGCGACCGGCTACCCCTCCGGGCTCCGTCATCTGAGCCCACTTCAATCAGAGAGTT 1020
Db 961 CTCGCGACCGGCTACCCCTCCGGGCTCCGTCATCTGAGCCCACTTCAATCAGAGAGTT 1020

QY 1021 GCTCTGTCACTACCGAGAGATCCCTTTATAGGCAAGCTATTCCTTTGAGCAATT 1080
Db 1021 GCTCTGTCACTACCGAGAGATCCCTTTATAGGCAAGCTATTCCTTTGAGCAATT 1080

QY 1081 AAGGGGGGAGACATCTTCTTCTGCACTCAAGAAAGAAAGTGGAGAGAGTCCCGCA 1140
Db 1081 AAGGGGGGAGACATCTTCTTCTGCACTCAAGAAAGAAAGTGGAGAGAGTCCCGCA 1140

QY 1141 AAACGTGTGCGGTTGGGCGTCAATGCGGTGCTTACCGGCGCTTGAATGTGCCGTC 1200
Db 1141 AAACGTGTGCGGTTGGGCGTCAATGCGGTGCTTACCGGCGCTTGAATGTGCCGTC 1200

QY 1201 ATCCGACCAATGTGTGATGCTGTGTGCAACCTGACCGCTTATGACCGGCTTTAC 1260
Db 1201 ATCCGACCAATGTGTGATGCTGTGTGCAACCTGACCGCTTATGACCGGCTTTAC 1260

QY 1261 GGCGACTTCAATGGGTATGACTGCAACAGTGTGTCAACCCAGACAGTGTGACTTACG 1320
Db 1261 GGCGACTTCAATGGGTATGACTGCAACAGTGTGTGTCAACCCAGACAGTGTGACTTACG 1320

QY 1321 CTGACCTTACCTTCAACATTTGAGCAATCAAGCTTCCCGAGAGTGTCTCCGCTACT 1380
Db 1321 CTGACCTTACCTTCAACATTTGAGCAATCAAGCTTCCCGAGAGTGTCTCCGCTACT 1380

QY 1381 CAACGTGCGGGTGAAGCTGCGAGAGGAGGACGAGGATCTACAGATTTGTGCGACCGGG 1440
Db 1381 CAACGTGCGGGTGAAGCTGCGAGAGGAGGAGGACGAGGATCTACAGATTTGTGCGACCGGG 1440

QY 1441 GAGGCTCTTCTTGGCATTTGACTGTGTCTCTGTGCGAGTGTATGAGCGGGGTTGT 1500
Db 1441 GAGGCTCTTCTTGGCATTTGACTGTGTCTCTGTGTGAGTGTATGAGCGAGGCTGT 1500

1501 GCTGTGATGAGCTTACGCCCGCCGAGACCAAGTTAGGCTACGAGCATACATGAACACC 1560
1501 GCTTGTATGAGCTTACGCCCGCCGAGACCAAGTTAGGCTACGAGCATACATGAACACC 1560
1561 CCGGGAATTCCCGTGTGCGCAAGACCAATCTGTAATTTTGGAGGCGCTTTTACGGGCTGC 1620
1561 CCGGGGCTTCCCGTGTGCGCAAGACCAATCTGTAATTTTGGAGGCGCTTTTACGGGCTGC 1620
1621 ACCCATATGAGAGCCCACTTCTATCCGACAAAGAGGAGGAGAAACCTTCCCTAT 1680
1621 ACTCATATATGAGAGCCCACTTCTATCCGACAAAGAGGAGGAGAAACCTTCCCTAT 1680
1681 CTGTAGCTGACCAAGCCACCGTGTGCGCTAGAGCTCAAGCCCTTCCCGCTGTGAGAC 1740
1681 CTGTAGCTGACCAAGCCACCGTGTGCGCTAGAGCTCAAGCCCTTCCCGCTGTGAGAC 1740
1741 CAGATGTGAGAGTGTGATGCTGCTCAAGCCCACTTCATGTGGCCAAACCCCTGCTA 1800
1741 CAGATGTGAGAGTGTGATGCTGCTCAAGCCCACTTCATGTGGCCAAACCCCTGCTA 1800
1801 TATTAAGCTGGGCGCTGTCCAGATATGAATCAACCTTGAACCCCACTCAAGATATATC 1860
1801 TATTAAGCTGGGCGCTGTCCAGATATGAATCAACCTTGAACCCCACTCAAGATATATC 1860
1861 ATGACATGATGTGCGCTGACCTGAGAGTGTGTCAAGAGTACCTGGGTGCTGTTGGCGGC 1920
1861 ATGACATGATGTGCGCTGACCTGAGAGTGTGTCAAGAGTACCTGGGTGCTGTTGGCGGC 1920
1921 GTTGTGCTGCTTTGGCGCGATGCTATCCACAGAGTGTGCTCAATGATAGGTAG 1980
1921 GTTGTGCTGCTTTGGCGCGATGCTATCCACAGAGTGTGCTCAATGATAGGTAG 1980
1981 ATTGTCTTCCGGGAAAGCCGCAATCATACCCGACAGAGGAGTCTCTTACCGGAGTTC 2040
1981 ATTGTCTTCCGGGAAAGCCGCAATCATACCCGACAGAGGAGTCTCTTACCGGAGTTC 2040
2041 GATGAATGGAAGATGC 2058
2041 GATGAATGGAAGATGC 2058

RESULT 14
US-09-238-076-5
Sequence 5, Application US/09238076
Patent No. US20020102540A1
GENERAL INFORMATION:
APPLICANT: RICE, CHARLES et al.
TITLE OF INVENTION: FUNCTIONAL DNA CLONE FOR HEPATITIS C
TITLE OF INVENTION: VIRUS (HCV) AND USES THEREOF
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MO
COUNTRY: USA
ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/238,076
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/034,756
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 6029-4831

TELECOMMUNICATION INFORMATION:
TELEPHONE: 314-727-5188
TELEFAX: 314-727-6092
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 12980 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-238-076-5

Query Match 86.1%; Score 1774.8; DB 3; Length 12980;
Best Local Similarity 91.4%; Pred. No. 0; Mismatches 177; Indels 0; Gaps 0;
Matches 1881; Conservative 0; Mismatches 177; Indels 0; Gaps 0;

2 TGGCCCTATGACGCGCTATGCGCCAGACAGAGGAGGCTTTTGGATGATATACCA 61
3418 TGGCCCTATGACGCGCTATGCGCCAGACAGAGGAGGCTTTTGGATGATATACCA 3477
62 GCTTGAACCGCGCGGACAAAAACAGGTGAGAGGTGAGGTTCAATGCTGTCACTGCTG 121
3478 GCTTGAACCGCGCGGACAAAAACAGGTGAGAGGTGAGGTTCAATGCTGTCACTGCTG 3537
122 CCCAATCTTCTTGGCAACCTGCAATTAACGGGGTGTGTTGACCTGTCTTACATGAGCGC 181
3538 CCCAATCTTCTTGGCAACCTGCAATTAACGGGGTGTGTTGACCTGTCTTACATGAGCGC 3597
182 GAACAAGACCAATTCGCTACCTTAAGAGTCTGTTATCAGATGATACCAATGTGAC 241
3538 GAACAAGACCAATTCGCTACCTTAAGAGTCTGTTATCAGATGATACCAATGTGAC 3657
242 AAGACCTGTGAGGTGAGCGCGCTGCTCCCAAGGTGCGCTCATTAACACCATGCACTTGG 301
3658 AAGACCTGTGAGGTGAGCGCGCTGCTCCCAAGGTGCGCTCATTAACACCATGCACTTGG 3717
302 GCTCTCTCGGACCTTTAATCTGTGTACAGAGGACCGCGATGATATTCCTGTGCGCGACGG 361
3718 GCTCTCTCGGACCTTTAATCTGTGTACAGAGGACCGCGATGATATTCCTGTGCGCGACGG 3777
362 GTGATGAGAGGAGGAGCGCTGCTTTGCGCCCGGCTATCTCTTACTTGAAGGCTCTCGG 421
3778 GTGATGAGAGGAGGAGCGCTGCTTTGCGCCCGGCTATCTCTTACTTGAAGGCTCTCGG 3837
422 GAGGCGCTGTGCTGTGCGCGCGAGACATGCGGTAGGATATTCAGAGCGCGGTATGCA 481
3838 GAGGCGCTGTGCTGTGCGCGCGAGACATGCGGTAGGATATTCAGAGCGCGGTATGCA 3897
482 CCCGTGAGAGTGTAAAGCGGTGACCTTATCCCGTGAAGAGCTTAAGACCAACATGA 541
3898 CCCGTGAGAGTGTAAAGCGGTGACCTTATCCCGTGAAGAGCTTAAGACCAACATGA 3957
542 GGTCCCGGATGTTCTCAGACAACTCTCCCGACAGAGTGCCTCCAGACTTCAAGTGG 601
3958 GGTCCCGGATGTTCTCAGACAACTCTCTTCCACAGAGTGCCTCCAGACTTCAAGTGG 4017
602 CCCACCTGATGCTTCCACCGGACGAGGTGAAGAGCAAGAGTCCCGGCGGATACGAG 661
4018 CCCACCTGATGCTTCCACCGGACGAGGTGAAGAGCAAGAGTCCCGGCGGATACGAG 4077
662 CTCAGGGCTACAAAGTGTGTGTCTCAACCCCTCGGTGTCTGCAACATGGGCTTTGGTG 721
4078 CCCAGGGCTACAAAGTGTGTGTCTCAACCCCTCGGTGTCTGCAACATGGGCTTTGGTG 4137
722 CTTAATGCTCAAGGCGCATGGGATTTGATCTTAATCATGAGAGCTGGGTGAGACAATTA 781
4138 CTTAATGCTCAAGGCGCATGGGATTTGATCTTAATCATGAGAGCTGGGTGAGACAATTA 4197
782 CTACTGAGACCCGATCAAGTATTCACCTTACGAGAGTTCCTTGCAGCGCGGCTGTT 841
4198 CCATGTGAGCGCCATCAAGTATTCACCTTACGAGAGTTCCTTGCAGCGCGGCTGTT 4257

| | | | |
|----|------|---|------|
| Db | 3538 | CCCAACCTTCTGTGGCAACGTGCATCAATTGGGGTATGCTGACCTGTCTTACCAACGGGGCCG | 3597 |
| Oy | 182 | GAAACAAGACCAATTCGTCACCTAAGGGTCTGTATCCAGATGTACAACAATGTGACC | 241 |
| Db | 3598 | GAAAGAGGACCATGCGATCACCAAGGGGCTGTATCCAGATGTATACAAATGTGACC | 365 |
| Oy | 242 | AAGACTGTGAGGCTGGCCGCTCCCAAGGTGCCGCTATTAAACCAATGCATTGGC | 301 |
| Db | 3658 | AAGACTTGTGTGGCTGGCCGCTCCTCAAGGTTCCCGCTCATGTGACACCTTCACCTCGC | 3717 |
| Oy | 302 | GCTCCTGGGACCTTTACCTGTCACAGAGGACGGCAGTCAATTCCTGTGGCCGACGGG | 361 |
| Db | 3718 | GCTCCTGGGACCTTTACCTGTCACAGAGGACGGCAGTCAATTCCTGTGGCCGACGGG | 3777 |
| Oy | 362 | GTGATGAGAGGGGCAAGCTGTCTTTCGCCCCGCTATCTCTTAATCTTGAAGGCTCTCGG | 421 |
| Db | 3778 | GTGATGAGAGGGGATGACCTGCTTTCGCCCCGCTATCTCTTAATCTTGAAGGCTCTCGG | 3833 |
| Oy | 422 | GAGCCCTCTGCTGTGGCCCCCGAGACATGCCGTAGGACATTTACAGCCCGGATGCA | 481 |
| Db | 3838 | GAGGCTCCCTGTGTGGCCCCCGAGACATGCCGTAGGACATTTACAGCCCGGATGTC | 3897 |
| Oy | 482 | CCCGTGAGATGGCTTAAGCGGGGACCTTCAATCCCGGTAGAGCTTTAAGACAAACATGA | 541 |
| Db | 3898 | CCCGTGAGATGGCTTAAGCGGGGACCTTCAATCCCGGTAGAGACCTTAAGACAAACATGA | 3957 |
| Oy | 542 | GATCCCCGGTGTCTCAGACAACTCTCCGCCACAGATGCCCGAGACTTACCAAGTGG | 601 |
| Db | 3958 | GATCCCCGGTGTCTCAGACAACTCTCTCCACAGAGATGCCCGAGACTTCCAGATGG | 4017 |
| Oy | 602 | CCCACTGCATGCTCCCAACCGGACGGGTAAAGACCAAGGTCCCGGCCGATACGACG | 661 |
| Db | 4018 | CCCACTGCATGCTCCCAACCGGACCGGTAAAGACCAAGGTCCCGGCTGGTACGACG | 4077 |
| Oy | 662 | CTCAGGGCTTAAAGGTGCTGTGTCTCAACCCCTCCGTTGTCTGACAAATGGGCTTTGGTG | 721 |
| Db | 4078 | CCCAAGGCTTAAAGGTGTGTGTGTCAACCCCTCTGTGTCTGCAACGCTGGGCTTTGGTG | 4137 |
| Oy | 722 | CTTACATGTCCAAAGGCCCATGGGATTTGAATCTTAATCATGAGACTGGGGTGAAGACAATTA | 781 |
| Db | 4138 | CTTACATGTCCAAAGGCCCATGGGGTGTGATCTTAATATCAGACCGGGGTGAAGACAATTA | 4197 |
| Oy | 782 | CTACTGGACGCCGATCAAGTATTCACCTACGCGAAGTTCCTTGCAGACGGCGGGTGT | 841 |
| Db | 4198 | CCACTGGACGCCCATCAAGTATCTCACTTAAGGCAAGTTCCTTGCAGACGGCGGGTGTCT | 4257 |
| Oy | 842 | CAGGGGGTGTATTATGACATTAATTTGTGACGAGTGCCACTCCAGATGCACATCA | 901 |
| Db | 4258 | CAGGAGGTGTATTATGACATTAATTTGTGACGAGTGCACACTCCAGATGCACATCA | 4317 |
| Oy | 902 | TCTTGGGATTTGGGACGTGCTCTTGAACAAAGAGACCGCGGGGGGAGACTGATGGC | 961 |
| Db | 4318 | TCTTGGGATTTGGGACGTGCTCTTGAACAAAGAGACGTGCGGGGGGAGACTGATTTGGC | 4377 |
| Oy | 962 | TGCGACCGCTAACCCCTCGGGGCTCCGTCACTGTGCCCATCTTAACATCGAGAGTTG | 1021 |
| Db | 4378 | TGCGACCTGTACCCCTCGGGGCTCCGTCACTGTGTCCCATCTTAACATCGAGAGTTG | 4437 |
| Oy | 1022 | CTGTGTCCAATAACGAGAGATCCCTTTTATGTGCAAGGCTAATTCCTTTGAAGCAATTA | 1081 |
| Db | 4438 | CTGTGTCCAACCAACGAGAGATCCCTTTTATGCGGCAAGGCTAATTCCTTCGAGGTATCA | 4497 |
| Oy | 1082 | AGGGGGGAGACATTCATCTTTCTGACACTGAAABAAGTGCGACGAGCTCGCGGGA | 1147 |
| Db | 4498 | AGGGGGGAGACATTCATCTTTCTGACACTGAAABAAGTGCGACGAGCTCGCGGGA | 4557 |
| Oy | 1142 | AACTGTGCGTGTGGGCGCTCAATGCGGTGCTTAATACCGCGGCTTGTATGTCTGCTCA | 1201 |
| Db | 4558 | AGCTGTGCGATTTGGGACATCAATGCGGTGCTTACTTAACGCGGTCTTGAAGTCTGCTCA | 4617 |
| Oy | 1202 | TCCGACCAAGTGTGATCGTTGTGTGTGTGCAATGACGCCCTCATGACCGGCTTTACCG | 1261 |

| | | | |
|----|------|---|------|
| Db | 4618 | TCGCCAGCAGGAGGGAGATGTTGTCGTTCGTGTGAGCCAGATGCTCTATGACTGCGCTTAAACG | 4677 |
| Qy | 1262 | GCGACTTCGATTCGGTGTATGATCTGCAACAAGTGTGTCAACCGACAGTGTGACTTCAGCC | 1321 |
| Db | 4678 | GCGACTTCGATCTGTGTATGATGATGCAACAGTGTGTCTCAACAGTGCATTTTCAGCC | 4737 |
| Qy | 1322 | TTGACCCCTACCTTACCCATTTGAGCAATCAAGCTTCCCGAGAGTGTGTCTCCCGTACTC | 1381 |
| Db | 4738 | TTGACCCCTACCTTTATACCTTATGACCAACACAGCTTCCCGAGAGTGTGTCTCCAGAGATC | 4797 |
| Qy | 1382 | AACGTCGGGGTAGGACTTGACAGAGAGGAAGCCAGGCACTCTACAGATTTGTGGACCGGGG | 1441 |
| Db | 4798 | AACGCGGGGAGAGACTGGCAGGGGGAAGCCAGGCACTCTACAGATTTGTGGCACCGGGGG | 4857 |
| Qy | 1442 | AGCGCTCTTTGGGATGTTTGAATCTGTCGTCTCTGCGAGTGTATGACGGGGGTGTG | 1501 |
| Db | 4858 | AGCGCCCTTCGGGATGTTTGAATCTGTCGTCTCTGAGTGTATGACGGGGGTGTG | 4917 |
| Qy | 1502 | CTTGGTATGAGCTTACCGCCCGCCAGACCAACAGTTAGGTATACGAGCATATGAACACC | 1561 |
| Db | 4918 | CTTGGTATGAGCTACCGCCCGCCAGACTACAGTTAGGTATACGAGCGTATGAACACC | 4977 |
| Qy | 1562 | CGGACCTTCCCGTGTCCAGAGACCATTTGAATTTTGGAGGGGCTCTTTACGGGTCTCA | 1621 |
| Db | 4978 | CGGGGCTTCCCGTGTCCAGAGACCATTTGAATTTTGGAGGGGCTCTTTACGGGGCTCA | 5037 |
| Qy | 1622 | CCCACTATGACGCCCACTTCTATTCGCCAGACAAAGAGTGGGGAAAACTTCCCTATC | 1681 |
| Db | 5038 | CTCATATATGATGCCCACTTTCTATTCGCCAGACAAAGAGTGGGGAACTTTCTTATCC | 5097 |
| Qy | 1682 | TGTTAGCGCTACCAAGCCACCGTGTGTGCGCTAGAGCTCAAGCCCTTCCCGTGTGGAGCC | 1741 |
| Db | 5098 | TGTTAGCGCTACCAAGCCACCGTGTGTGCGCTAGAGGCTCAAGCCCTTCCCGTGTGGAGCC | 5157 |
| Qy | 1742 | AGATGTGGAATGCTGTGATTCGCTGTCAAGGCCCACTTCATGTGGGCCAAACACTGTGCAT | 1801 |
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| Qy | 1802 | ATTAGACTGGGCGCTGTCCAGATGATGACCTGTGACGCCACCAAGTCCCAAGTATATCA | 1861 |
| Db | 5218 | ACAAGCTGGGCGCTGTTCAGATGATGATCACCTGTGACGCCACCAATCAACCAATATATCA | 5277 |
| Qy | 1862 | TGACATGATATGTCCGCTGTACCTGTGAGGTGTCTCAAGATGATACCTGTGGGTCTCTTGGCGCG | 1921 |
| Db | 5278 | TGACATGATATGTCCGCGACCTGTGAGGTGTCTCAAGATGATACCTGTGGGTCTCTTGGCGCG | 5337 |
| Qy | 1922 | TTTCTGTGCTCTTTGGCGCGCTATTTGACCTATCAACAGCTGTGCTGTGATATGATATGATGA | 1981 |
| Db | 5338 | TCTGTGTGCTCTTGGCGCGCTATTTGCTGTCTGTCAACAGCTGTGCTGTGATATGATGAGGA | 5397 |
| Qy | 1982 | TTTGTCTTGTCCGGAAGCGCGGCAATCATACCGACAGGGAAATGCTCTTACCGGAGATTGCG | 2041 |
| Db | 5398 | TTTGTCTTGTCCGGAAGCGCGCAATTTATCTGTACAGGGAGATTCTTACCGAGAGTTTGG | 5457 |
| Qy | 2042 | ATTGAATGTGAAGATGCT 2059 | |
| Db | 5458 | ATTGAATGTGAAGATGCT 5475 | |

Search completed: February 7, 2006, 21:01:03
Job time : 1516 secs

1000 WORK (1000)

November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New).

Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

THE SPOON (aspio)

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 7, 2006, 20:11:03 ; Search time 400 Seconds
(without alignment) 4318.173 Million cell updates/sec

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Perfect score: 2061
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Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 6068529 seqs, 41903697 residues

Total number of hits satisfying chosen parameters: 12137058

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database: Published Applications NA New:

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11: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB_seq.*

Filed. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|------------------|--------------------|
| 1 | 1765.2 | 85.6 | 9599 | US-10-985-205-1 | Sequence 1, Appli |
| 2 | 1727.8 | 83.8 | 7983 | US-10-509-921-7 | Sequence 7, Appli |
| 3 | 1727.8 | 83.8 | 7989 | US-10-509-921-2 | Sequence 2, Appli |
| 4 | 1727.8 | 83.8 | 7992 | US-10-509-921-3 | Sequence 3, Appli |
| 5 | 1381.2 | 67.0 | 7848 | US-11-173-792-7 | Sequence 7, Appli |
| 6 | 1381.2 | 67.0 | 7979 | US-10-509-921-9 | Sequence 9, Appli |
| 7 | 1381.2 | 67.0 | 7979 | US-10-509-921-10 | Sequence 10, Appli |
| 8 | 1381.2 | 67.0 | 7980 | US-10-509-921-4 | Sequence 4, Appli |
| 9 | 1381.2 | 67.0 | 7980 | US-10-509-921-5 | Sequence 5, Appli |
| 10 | 1381.2 | 67.0 | 7987 | US-11-173-792-5 | Sequence 5, Appli |
| 11 | 1381.2 | 67.0 | 7987 | US-11-173-792-8 | Sequence 8, Appli |
| 12 | 1381.2 | 67.0 | 7987 | US-11-173-792-13 | Sequence 13, Appli |
| 13 | 1381.2 | 67.0 | 7989 | US-10-509-921-6 | Sequence 6, Appli |
| 14 | 1381.2 | 67.0 | 7989 | US-10-509-921-13 | Sequence 13, Appli |
| 15 | 1381.2 | 67.0 | 7989 | US-10-509-921-14 | Sequence 14, Appli |
| 16 | 1381.2 | 67.0 | 7989 | US-11-119-730-1 | Sequence 1, Appli |
| 17 | 1381.2 | 67.0 | 7989 | US-11-173-792-6 | Sequence 6, Appli |
| 18 | 1381.2 | 67.0 | 7989 | US-11-173-792-10 | Sequence 10, Appli |
| 19 | 1381.2 | 67.0 | 7992 | US-11-111-686-1 | Sequence 1, Appli |
| 20 | 1381.2 | 67.0 | 7992 | US-11-111-686-4 | Sequence 4, Appli |
| 21 | 1381.2 | 67.0 | 7992 | US-11-111-686-6 | Sequence 6, Appli |
| 22 | 1379.6 | 66.9 | 7989 | US-11-173-792-9 | Sequence 9, Appli |

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|----|--------|------|------|--------------------|--------------------|
| 23 | 1379.6 | 66.9 | 7992 | US-11-111-686-2 | Sequence 2, Appli |
| 24 | 1379.6 | 66.9 | 7992 | US-11-111-686-5 | Sequence 5, Appli |
| 25 | 1379.6 | 66.9 | 7995 | US-11-111-686-3 | Sequence 3, Appli |
| 26 | 1367.4 | 66.3 | 7979 | US-10-509-921-11 | Sequence 11, Appli |
| 27 | 1367.4 | 66.3 | 7979 | US-10-509-921-12 | Sequence 12, Appli |
| 28 | 1367.4 | 66.3 | 7989 | US-10-509-921-8 | Sequence 8, Appli |
| 29 | 1355.6 | 65.8 | 2841 | US-10-528-644A-51 | Sequence 51, Appli |
| 30 | 1351.6 | 65.6 | 2946 | US-10-528-644A-54 | Sequence 54, Appli |
| 31 | 137 | 6.6 | 225 | US-10-509-921-1 | Sequence 1, Appli |
| 32 | 128.4 | 6.2 | 162 | US-11-137-220-3 | Sequence 3, Appli |
| 33 | 44.6 | 2.2 | 1281 | US-10-454-437-255 | Sequence 255, App |
| 34 | 44.6 | 2.2 | 1281 | US-11-055-822-363 | Sequence 363, App |
| 35 | 42.2 | 2.0 | 3240 | US-11-052-554A-529 | Sequence 529, App |
| 36 | 36.8 | 1.8 | 2841 | US-10-528-644A-51 | Sequence 51, Appli |
| 37 | 36.8 | 1.8 | 2946 | US-10-528-644A-54 | Sequence 54, Appli |
| 38 | 36.6 | 1.8 | 2514 | US-11-052-554A-543 | Sequence 543, App |
| 39 | 36.6 | 1.8 | 7983 | US-10-509-921-7 | Sequence 7, Appli |
| 40 | 35.6 | 1.7 | 1119 | US-10-858-720-48 | Sequence 48, Appli |
| 41 | 35.6 | 1.7 | 2251 | US-11-094-519A-2 | Sequence 2, Appli |
| 42 | 35.6 | 1.7 | 2772 | US-11-052-554A-531 | Sequence 531, App |
| 43 | 35.6 | 1.7 | 3239 | US-11-094-519A-18 | Sequence 18, Appli |
| 44 | 35.4 | 1.7 | 5119 | US-11-108-528-61 | Sequence 61, Appli |
| 45 | 35.4 | 1.7 | 7979 | US-10-509-921-11 | Sequence 11, Appli |

ALIGNMENTS

| | | | | |
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| RESULT 1 | | | | |
| US-10-985-205-1 | | | | |
| ; Sequence 1, Application US/10985205 | | | | |
| ; Publication No. US20050266400A1 | | | | |
| GENERAL INFORMATION: | | | | |
| ; APPLICANT: Dumonceaux, Julie | | | | |
| ; APPLICANT: Cormier, Emmanuel G. | | | | |
| ; APPLICANT: Gardner, Jason P. | | | | |
| ; APPLICANT: Dreglic, Tatjana | | | | |
| ; TITLE OF INVENTION: NOVEL SEQUENCES ENCODING HEPATITIS C VIRUS GLYCOPROTEINS | | | | |
| ; FILE REFERENCE: 71242-A/IPW/AJD | | | | |
| ; CURRENT APPLICATION NUMBER: US/10/985,205 | | | | |
| ; CURRENT FILING DATE: 2004-11-09 | | | | |
| ; PRIOR APPLICATION NUMBER: US 60/519,536 | | | | |
| ; PRIORITY FILING DATE: 2003-11-12 | | | | |
| ; NUMBER OF SEQ ID NOS: 20 | | | | |
| ; SOFTWARE: PatentIn version 3.1 | | | | |
| ; SEQ ID NO 1 | | | | |
| ; LENGTH: 9599 | | | | |
| ; TYPE: DNA | | | | |
| ; ORGANISM: Hepatitis C virus | | | | |
| US-10-985-205-1 | | | | |
| Query Match | | | | |
| Best Local Similarity 91.1%; Pred. No. 0; | | | | |
| Matches 1875; Conservative 0; Mismatches 183; Indels 0; Gaps 0; | | | | |
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| QY | 62 | GCTTGACCGCGCGGACAAACAGGTGAGGCTGAGTTCAGTCTGTCACTGTG | 121 | |
| DB | 3478 | GCTTGACCGCGCGGACAAACAGGTGAGGCTGAGTTCAGTCTGTCACTGTG | 3537 | |
| QY | 122 | CCGACGCTTTGCGCACTGCAATTAACGCGGTGTGTTGACTGTCTTCAACGAGCC | 181 | |
| DB | 3538 | CCGACGCTTTGCGCACTGCAATTAACGCGGTGTGTTGACTGTCTTCAACGAGCC | 3597 | |
| QY | 182 | GAAAGGACGATGCGCTGCACTTAAGGCTCTGTTATCAGATGACCAATGGAAC | 241 | |
| DB | 3598 | GAAAGGACGATGCGCTGCACTTAAGGCTCTGTTATCAGATGACCAATGGAAC | 3657 | |
| QY | 242 | AAGAGCTGTAGGCTGCGCGCTCCCAAGGTGCGGCTCAATTAACATGCACTTGC | 301 | |

| | | | |
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| Db | 3658 | AAGACCTTGTGGGCTGGGCCCGCTCTCTCAAGGTTCCCGCTCAATTGACACCTGTACTGCG | 3717 |
| Qy | 302 | GCTCCTCGGACCTTTACCTGTGTACAGAGGACAGCCGATGTCAATTCTGTGGCGGACGGG | 361 |
| Db | 3718 | GCTCCTCGGACCTTTACCTGTGTACAGAGGACAGCCGATGTCAATTCTGTGGCGGCGAG | 3777 |
| Qy | 352 | GTGATGCGAGGGGCGAGCTGCTTTGGCCCGGCTTATCTTTACTTTGAAAGGCTCTCGG | 421 |
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| Qy | 422 | GAGGGCCCTGTGTGTGGCCCGGAGGACATGCGGTAGGGCATTTTCAGACCGCGGATATGA | 481 |
| Db | 3838 | GAGGGCCCTGTGTGTGGCCCGGAGGACAGCGGTAGGGCTTATTCAGAGCGCGGATGTGA | 3897 |
| Qy | 482 | CCCGTGTAGTGGCTTAAGCGGTGTGACCTTATCCCGGTAGAGGCTTAGAGCAACATGA | 541 |
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| Qy | 542 | GGTCCCCGGTGTTCACAGCAACTCTCTCCCAACAGAGTGGCCCAAGCTAACAGTG | 601 |
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| Db | 4018 | CCCACTGTGATGTCTCCACCGGCGAGGTTAAGAGACCAAGGTCCCGGCTGTACGAG | 4077 |
| Qy | 662 | CTCAGGGCTACAGAGGTGTGTGTCTCAACCCCTCGTGTCTGCAACAATGGGCTTTGGTG | 721 |
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| Qy | 722 | CTTACATGTCCAAAGGCCCATGGGATTTGATCCTAACATAGAGCTGGGTTAGAGCAATTA | 781 |
| Db | 4138 | CTTACATGTCCAAAGGCCCATGGGATTTGATCCTAACATAGAGCCGGGTTAGAACATTA | 4197 |
| Qy | 782 | CTACTGGGAGCCCCGATTCACGTATTCACCTACGGGAATTTCTTGGCGACGGCGGGTGT | 841 |
| Db | 4198 | CCACTGGGAGCCCCGATTCACGTATTCACCTACGGGAAGTTCTTGGCGACGGCGGGTGT | 4257 |
| Qy | 842 | CAGGGGGTGTATATACATTAATTAATTGTGACGAGTGGCACTCCAGGATCAACATCA | 901 |
| Db | 4258 | CAGGAGGTGTCTTATATGACATTAATTTGTGACGAGTGGCACTCCAGGATGCCACATCA | 4317 |
| Qy | 902 | TCTTGGGCAATTGGCACTGTCTTTCACCAAGCAGAGACCGCGGGGCGAGACTGATGTGC | 961 |
| Db | 4318 | TCTTGGGCAATTGGGCACTGTCTTTCACCAAGCAGAGACTGCGGGGGCGAGACTGATGTGC | 4377 |
| Qy | 962 | TGCGCAACGGCTACCCCTCGGGGCTCCGTACCTGTGTCGCCCATCTTAACATCGAGAGGTTG | 1021 |
| Db | 4378 | TGCGCACTGTCTAACCCCTCGGGGCTCCGTACCTGTGTCGCCCATCTTAACATCGAGAGGTTG | 4437 |
| Qy | 1022 | CTGTGTCCATCAACCGGAGAGATCCCTCTTTATGGGAAGGCTATTCCCTTGAAGCAATTA | 1081 |
| Db | 4438 | CTGTGTCCATCAACCGGAGAGATCCCTCTTTATGGGAAGGCTATTCCCTCGAGGTGATCA | 4497 |
| Qy | 1082 | AGGGGGGAGACATCTCATTTCTTGCACTCAAGAGAAGTGCAGCAGCTCGCGGCA | 1141 |
| Db | 4498 | AGGGGGGAGACATCTCATTTCTTGCACTCAAGAGAAGTGCAGCAGCTCGCGGCA | 4557 |
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| Db | 4558 | AGCTGTGTGCGAATTGGGCAATCAATGCCGTGTGCTTATCACCGGCTTGAATGTGTCCGTCA | 4617 |
| Qy | 1202 | TCCCGACCAAGTGTAGCGTGTGCGTGTGGCAACTGACGCGCTCATGACCGGCTTTACCG | 1261 |
| Db | 4618 | TCCCGACCAAGCGGCAATGTGTGCGTGTGCGAAGCGAGCTTCAATGACTGGCTTTACCG | 4677 |
| Qy | 1262 | GCGACTTGCATTCGGGTGATAGCTGCAACACGTGTGTCAACCGACAGTGTGACTTTCAGCC | 1321 |
| Db | 4678 | GCGACTTGCATCTGTGTGATAGCTGCAACACGTGTGTCACTGACAGACTGTATTTACGCC | 4737 |
| Qy | 1322 | TTGACCTTACCTTTCACCATTTGAGACATACGCTTTCGCCAGATGTGTCTTCCGTACTC | 1381 |
| Db | 4738 | TTGACCTTACCTTTCACATTTGAGACACACGCTTCCCGAGATGTGTCTTTCACAGACTC | 4797 |

| | | | |
|----|------|---|------|
| QY | 1382 | AACGTCCGGGATAGACATGCGCAGAGGGAAGCCAGGCACTTACAGATTTTGTGGCACCGGGGG | 144 |
| Db | 4798 | AACCCCGGGGAGAGACATGGCAGGGGGGAAGCCAGGCACTTAATGATTTGTGGCACCGGGGG | 485 |
| QY | 1442 | AGCGTCCTTCTGGGATGTTTGACTCGATCTGCTCTGCGGATGCTATGACCGGGGTTGTG | 1501 |
| Db | 4858 | AGCCGCCCTCCGGGATGTTGCACTGTCGCTCTCTGAGATGCTATGACCGGGGCTGTG | 4917 |
| QY | 1502 | CTTGATATGACTTACCGCCGGCCGAGACACAGATTAGGCTACGAGCATACATGAACACC | 1561 |
| Db | 4918 | CTTGATATGAGACTCAGCCGCCCGACGACTACAGTTAGGCTACGAGCGTACATGAACACC | 4977 |
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| Db | 5038 | CTCATATATGAGAGCCCACTTTTATTCGACAGACAAAGCAGATGGGGAGAACTTCTTAC | 5097 |
| QY | 1682 | TGATAGGCTACCAAGCCACCGGTGGCGCTAGAGCTCAAGGCCCTCCCGGTGGAGAC | 1741 |
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| Db | 5158 | AGATGTGGAATGTTTGAATCCGCTTAAACCACTTCATGGGCAACACTCTGCTAT | 5217 |
| QY | 1802 | ATTAACATGGGGGCGCTGCCAAGATGAAGTACACCTGACGACACCAATCCAAATATCA | 1861 |
| Db | 5218 | ACAGATCGGGGCGCTGTGTAGATATGATAGTACACCTGACGACACCAATCCAAATATCA | 5277 |
| QY | 1862 | TGACATGATATCGAGCTGACCTGAGAGGTGCTCAGAGATACCTGGGTGCTGTTGGCGCG | 1921 |
| Db | 5278 | TGACATGATATCGAGCTGACCTGAGAGGTGCTCAGAGATACCTGGGTGCTGTTGGCGCG | 5333 |
| QY | 1922 | TTCTGGGCTCTTTGGCCGCGGTAATGGCTATCAACAGGCTGGGTGTCTAATGATAGGA | 1981 |
| Db | 5338 | TTCCTGGGCTCTGAGCCGCGGTAATGGCTATCAACAGGCTGGGTGTCTAATGATAGGA | 5397 |
| QY | 1982 | TTGTCTTGTCCGGAAGCCGCGCAATCATACCCGACAGGGAAGTCTCTACCGGGAGTTG | 2044 |
| Db | 5398 | TGCTCTTGTCCGGAAGCCGCGCAATTAATCTGACAGGGAAGTCTCTACCAAGAGTTG | 5455 |
| QY | 2042 | ATGAATGGAAGAGTGCT 2059 | |
| Db | 5458 | ATGAGATGGAAGAGTGCT 5475 | |

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RESULT 2
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; Sequence 7, Application US/10509921
; Publication No. US20050250093A1
; GENERAL INFORMATION:
; APPLICATION: SmithKline Beecham Corporation
; TITLE OR INVENTION: Hepatitis C Virus Sub-Genomic Replicons
; FILE REFERENCE: PS1335
; CURRENT APPLICATION NUMBER: US/10/509,921
; CURRENT FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: 60/369,685
; PRIOR FILING DATE: 2002-04-03
; NUMBER OF SEQ. ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ. ID NO. 7
; LENGTH: 7983
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HCV 1a Rep1cons
US-10-509-921-7

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Query Match 83.8%; Score 1727.8; DB 7; Length 7983;
Best Local Similarity 89.9%; Pred. No. 0;
Matches 1852; Conservative 0; Mismatches 207; Indels 0; Gaps 0;

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DB 1801 ATGGCGCTTATTACGGCTTACCTCCACAGACAGAGGCTTACCTTGGCTGATCATCACT 1860
QY 61 AGCTTGACCGGCGGGGAGCAAAAACAGAGTGAAGGTTGAGTTCAAGATGCTCACTGCT 120
DB 1861 AGCTTGACAGGCGGGGAGCAAGAACAGAGTGAAGGTTGAGTTCAAGATGCTTCCACCGCA 1920
QY 121 GCCCAGACTTTCTTGGCAACCTGATTAACGAGGAGTGTGTTGAGACTGTCTACATGAGACC 180
DB 1921 ACACAAATTTTCTGCTGACACTGCTCAATGAGCGTGTGTTGAGACTGTCTATCATGAGTCC 1980
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QY 241 CAAGACTCTGATAGGCTGGCGCGCTCCCAAGTGGCGCGCTATTAAACATGACATTCG 300
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DB 2101 GGCTCTGAGACCTTTACCTGATGACAGAGGACGCGGATGTCATTCTGTGGCGCGAGG 2160
QY 361 GGATGATGACAGGAGGAGCGCTGTTCGCGCGCGCTATCTCTTAACTTGAAGAGCTCTCG 420
DB 2161 GGATGATGACAGGAGGAGCGCTGTTCGCGCGCGCTATCTCTTAACTTGAAGAGCTCTCG 2220
QY 421 GAGAGGCTCTGCTGTGTGCGCGAGAGACATGCGGTAGGACATTTAGAGCGCGGTATGC 480
DB 2221 GAGAGGCTCTGCTGTGTGCGCGAGAGACATGCGGTAGGACATTTAGAGCGCGGTATGC 2280
QY 481 ACCCGTGAAGTGGCTTAAGGCGGTGACTTCAATCCCGTGAAGAGCTTGAAGCAACGAC 540
DB 2281 ACCCGTGAAGTGGCTTAAGGCGGTGACTTCAATCCCGTGAAGAGCTTGAAGCAACGAC 2340
QY 541 AGGTCCCGGCTGTCTCAGACAACTCTCCCAACAGAGTGGCCCAAGTACCAAGT 600
DB 2341 AGGTCCCGGCTGTCTCAGAGCAACTCTCCCAACAGAGTGGCCCAAGTACCAAGT 2400
QY 601 GCCCACTGATGCTCCCAACGCGGTAAAGACCAAGTCCCGCGCATACCA 660
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QY 841 TCAGGGGCTGCTTAAGATATAATTTGTGACAGTGCCTTCCAGAGTGCACATCC 900
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DB 2701 ATCTTGGGCAATTTGCACTGTCTTTGACCAAGAGAGACCTGCGGGGCGAGACTGACTGTG 2760
QY 961 CTGCGCACCGCTACCCCTTCGGGCTTCGCTCACTGTGCTCCCATCTTAACATGAGAGGTT 1020
DB 2761 CTGCGCACCTGCTACCCCTTCGGGCTTCGCTCACTGTGCTCCCATCTTAACATGAGAGGTT 2820
QY 1021 GCTGTGTCACTACCGAGAGATCCCTTTTATGCAAGGCTATTCCTCTTGAAGCAAT 1080

DB 2821 GCTGTGTCACTACCGAGAGATCCCTTTTACGCGCAAGGCTATCCCTCGAGGTGATC 2880
QY 1081 AAGGGGGAGACATCTCATCTTCTGCGCATCTCAAGAAAGTGTGACGAGCTGCGCGCA 1140
DB 2881 AAGGGGGAGACATCTCATCTTCTGCGCATCTCAAGAAAGTGTGACGAGCTGCGCGCG 2940
QY 1141 AACTGTGTGCGGTTGGGCGTCAATGCGGTGCTTACAGCGGCGCTTATGATGTGCGTC 1200
DB 2941 AACTGTGTGCGGTTGGGCGTCAATGCGGTGCTTACAGCGGCGCTTATGATGTGCGTC 3000
QY 1201 ATCCGACCAAGTGTGACGTTGTGCTGCTGCGCAACTGACGCGCTCATATGACGCGCTTAC 1260
DB 3001 ATCCGACCAAGGCGGAGATGCTGTGTGTGTGTCAGACATGCTCATATGACGCGCTTAC 3060
QY 1261 GGCGACTTGAATTTGGGTATGACTGCAACAGCTGTGTACCCAGACAGTGTGACTTACG 1320
DB 3061 GGCGACTTGAATTTGGGTATGACTGCAACAGCTGTGTCACTAGACAGTGTGACTTACG 3120
QY 1321 CTGACCCCTTACCTTCAACATGAGACATCAAGGCTTCCAGAGTGTGCTCCGCTACT 1380
DB 3121 CTGACCCCTTACCTTCAACATGAGACATCAAGGCTTCCAGAGTGTGCTCTCAGAGACT 3180
QY 1381 CAAGTCTGGGTTAGACTGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1440
DB 3181 CAAGTCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3240
QY 1441 GAGCGCTCTTGTGAGATGTTGACTGTGTGTCTCTGCGAGTGTGATGACGCGGCTGT 1500
DB 3241 GAGCGCGCTCTGCGAGATGTTGACTGTGTGTCTCTGCGAGTGTGATGACGCGGCTGT 3300
QY 1501 GCTTGTATGAGCTTATGCGCGCGCGAGACCAAGTGGGCTTACAGACATATGAAACACC 1560
DB 3301 GCTTGTATGAGCTTATGCGCGCGCGAGACCTTACAGTATGAGCTTACAGACATGAAACACC 3360
QY 1561 CCGGAGCTTCCCGTGTGCGCAAGACCATTTGAATTTTGGAGGCGTCTTTACGCGCTC 1620
DB 3361 CCGGAGCTTCCCGTGTGCGCAAGACCATTTGAATTTTGGAGGCGTCTTTACGCGCTC 3420
QY 1621 ACCCATATGAGCGCCCATCTCTATCCAGACAAAGACAGATGGGAGAAACCTTCTAT 1680
DB 3421 ACTCATATGATGAGCCCATCTTTTATCCAGACAAAGACAGATGGGAGAAACCTTCTAT 3480
QY 1681 CTGTGATGATCAAGCCACCGTGTGCGTGAAGTCAAGCCCTCCCGCGTGGGAGAC 1740
DB 3481 CTGTGATGATCAAGCCACCGTGTGCGTGAAGTCAAGCCCTCCCGCGTGGGAGAC 3540
QY 1741 CAGATGTGAAGTCTTGATCCGTCTCAAGGCCAACCTCCATGGGCGCAACCTTGTGCTA 1800
DB 3541 CAGATGTGAAGTCTTGATCCGTCTCAAGGCCAACCTCCATGGGCGCAACCTTGTGCTA 3600
QY 1801 TATAGACTGGCGCTGTCCAGAAATGAAGTCAACCTTGAAGCAGCAGGATCAAGATATATC 1860
DB 3601 TATAGACTGGCGCTGTCCAGAAATGAAGTCAACCTTGAAGCAGCAGGATCAAGATATATC 3660
QY 1861 ATGACATGATGTGGGCTGACCTGAGAGTGTCTCAAGATACCTGGGTCTGTGGCGCG 1920
DB 3661 ATGACATGATGTGGGCTGAGCCTGAGAGTGTCTCAAGATACCTGGGTCTGTGGCGCG 3720
QY 1921 GTTCTGGCTCTTTGGCGCGGCTATTTGCTTCCAGAGGCTGCTGTATGATGAGTATG 1980
DB 3721 GTTCTGGCTCTTTGGCGCGGCTATTTGCTTCCAGAGGCTGCTGTATGATGAGTATG 3780
QY 1981 ATTTGCTTGTGCGGAAAGCGGCAATCAATCCGACAGGAGAGTCTCTACCGGAGTTTC 2040
DB 3781 ATTTGCTTGTGCGGAAAGCGGCAATCAATCCGACAGGAGAGTCTCTACCGGAGTTTC 3840
QY 2041 GATGAATGAGAGTGTCT 2059
DB 3841 GATGAATGAGAGTGTCT 3859

RESULT 3

```
US-10-509-921-2
; Sequence 2: Application US/10509921
; Publication No. US20050250093A1
; GENERAL INFORMATION:
; APPLICATION: SmithKline Beecham Corporation
; TITLE OF INVENTION: Hepatitis C Virus Sub-genomic Replicons
; FILE REFERENCE: P51335
; CURRENT APPLICATION NUMBER: US/10/509,921
; CURRENT FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: 60/369,685
; PRIOR FILING DATE: 2002-04-03
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 7989
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The polynucleotide sequence encodes sequences from
; OTHER INFORMATION: HCV H77 (BB7-F1) Replicons
US-10-509-921-2

Query Match      83.8%; Score 1727.8; DB 7; Length 7989;
Best Local Similarity 89.9%; Pred. No. 0;
Matches 1852; Conservative 0; Mismatches 207; Indels 0; Gaps 0;

QY      1  ATGGGCGCTATACAGCGCCCTATGCGCCAGACAGAGGGCGCTTTGGAGTGCATATACCC 60
DB      1801  ATGGGCGCTATTATACGCGCTTACTCTCCAAACAGACGCGAGGCTTACCTGGCTGCATCATCT 1860
QY      61  AGCTTGACCGCGCGGGGACAAACAAACAGGTGAGGGGTGAGGTTCAAGTCTGTCACTGCT 120
DB      1861  AGCTTCACAGCGCGGGGACAGAAACAGGTGAGGGGAGTCCAGTGTCTCCACCGCA 1920
QY      121  GCCCAAGCTTCTTGGCAACCTGCAATTAAAGGGGTGTGTGGACGTGTCTACCATGAGGC 180
DB      1921  ACACATATCTTCTCTGGCGACCTGCGTCATAGGCGTGTGTGGACGTGTCTATCATGTGTC 1980
QY      181  GGAACAGAGCATTTGGCTGCTACCTTAAGGGTCTGTATTACAGATGTACACCAATGTGAC 240
DB      1981  GGCTCAAAAGACCTTGGCGGCGCCAAAGGGCCCAATACCAAAATGTACCAATGTGAC 2040
QY      241  CAAGAAGCTGTAGGTGCGCGCTCCCAAGGTGCGCGCTCATTTAAACCATGACCTTGC 300
DB      2041  CAAGAAGCTTGTGGGTGCGCGCTCCCTCAAGGTTCCTCGTCAATGACACCTGTACCTGC 2100
QY      301  GGCCTCTGGGACCTTTACTGTGTACAGAGGACAGCCGATGTCAATTCGTGTGCGCGAGCG 360
DB      2101  GGCTCTCTGGGACCTTTACTGTGTGTACAGAGGACAGCCGATGTCAATTCCTGTGCGCGAG 2160
QY      361  GGTGATGGAGGGGAGCGCTTTCGCGCGCGCTATCTTACTTTGAAAGGCTCTCG 420
DB      2161  GGTGATGAGGGGAGCGCTTTCGCGCGCGCTATCTTACTTTGAAAGGCTCTCG 2220
QY      421  GGAGGCGCTCTGTGTGCGCGCAGAGACATGCGTATGAGCATTTGAGAGCGCGGTATGC 480
DB      2221  GGGGGTCTCTGTGTGTGCGCGCGCGAGACAGCGGTGAGCATTTGAGAGCGCGGTATGC 2280
QY      481  ACCCGTGAAGTGGCTAAGCGGTGACCTTCATCTCCCGTGAAGAGCTTGAAGCAACATG 540
DB      2281  ACCCGTGAAGTGGCTAAGCGGTGAGCTTATCTCGTGAAGAACTTGAAGCAACATG 2340
QY      541  AGGTCCCGGTGTCTCAACAACATCTCTCCCAAGAGAGTGCCTCCAGAGCTTCAAGTG 600
DB      2341  AGATCCCGGTGTCTCAAGCAACATCTCTCCCAAGAGAGTGCCTCCAGAGCTTCAAGTG 2400
QY      601  GCCCACTGTGATCTCCCAAGCGGAGGTGAAGAGCAAGAGTCCCGGCGCATACGA 660
DB      2401  GCCCACTGTGATCTCCCAAGCGGAGGTGAAGAGCAAGAGTCCCGGCGCATACGA 2460
QY      661  GCTGAGGGGTACAGAGTGTGTGTCAACCCCTTCGTTGTGCAACAATGGGCTTTGGT 720
DB      2461  GCCCAAGGGGTACAGAGTGTGTGTCAACCCCTTCGTTGTGCAACGCTGGGCTTTGGT 2520
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QY      721  GCTTACATGTCCAAAGGCCCATGGGATTTGATCTTAACATCAGAGACTGGGGTGAACAATT 780
DB      2521  GCTTACATGTCCAAAGGCCCATGGGATTTGATCTTAATACAGAGCCGGGGTGAACAATT 2580
QY      781  ACTACTGGACCGCGATCAGCTATTCACCTACCGCAAGTTCTTTCGCGACGGCGGTGT 840
DB      2581  ACGACTGGACCGCGATCAGCTATTCACCTACCGCAAGTTCTTTCGCGACGGCGGTGT 2640
QY      841  TCAGGGGTGTGTATGACATTAATTTGTGACAGGTGTCCACTCCAGAGTGAACATCC 900
DB      2641  TCAGAGGTGTGTATGACATTAATTTGTGACAGGTGTCCACTCCAGAGTGTCCATCC 2700
QY      901  ATCTTGGGCAATTTGGACATCTGTCTTGAACCAAGAGAGACGCGGGGCGAGACTGTG 960
DB      2701  ATCTTGGGCAATTTGGACATCTGTCTTGAACCAAGAGAGACTGTGCGGGGCGAGACTGTG 2760
QY      961  CTCGCAACCGGTACCCCTCCGGGCTCGTCACTGTGCCCATTCCTAACATCGAGAGTT 1020
DB      2761  CTCGCACTGTACCCCTCCGGGCTCGTCACTGTGTCCATCTTAACATCGAGAGTT 2820
QY      1021  GCTGTGTCACTTACCGGAGAGATCCCTTTTATGCGAAGCTATTCCTTGAACAAAT 1080
DB      2821  GCTGTGTCACTTACCGGAGAGATCCCTTTTATGCGAAGCTATTCCTTGAAGTATC 2880
QY      1081  AAGGGGGGAGACATCTCATCTTCTGCACTCAAAAGAAAGTGGACGAGCTCGCGCA 1140
DB      2881  AAGGGGGGAGACATCTCATCTTCTGCACTCAAAAGAAAGTGGACGAGCTCGCGCG 2940
QY      1141  AAACGTGTGCGTGGGGGTCAATGCGTGGCTTACCTACCGGAGCTTGAATGTCTGTC 1200
DB      2941  AAGCTGTGTGATGGGATCAATGCGTGGCTTACCTACCGGAGCTTGAATGTCTGTC 3000
QY      1201  ATCCGACCATGTGTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1260
DB      3001  ATCCGACCATGTGTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3060
QY      1261  GGGGACTTGTGATGGATGTGACTGCAACAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1320
DB      3061  GGGGACTTGTGATGGATGTGACTGCAACAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3120
QY      1321  CTGACCCCTTACCTTACCATTTAGACATACAGCTTCCCGAGATGCTGTCTCCGTACT 1380
DB      3121  CTGACCCCTTACCTTACCATTTAGACATACAGCTTCCCGAGATGCTGTCTCCAGACT 3180
QY      1381  CAGGTGTGGGTGAGACTGTGCAAGAGGAAAGCCAGGCACTTACAGATTTGTGTGCA 1440
DB      3181  CAGGTGTGGGTGAGACTGTGCAAGAGGAAAGCCAGGCACTTACAGATTTGTGTGCA 3240
QY      1441  GAGGCTCTTCTGTGATTTTGAATCTGTGTCTCTGTGAGTGTGTATGACGCGGGTGT 1500
DB      3241  GAGGCTCTTCTGTGATTTTGAATCTGTGTCTCTGTGAGTGTGTATGACGCGGGTGT 3300
QY      1501  GCTTGTATGACTTACCGCGCGCGAGACCAACATTTAGGCTTACGAGCATATGAAAC 1560
DB      3301  GCTTGTATGACTTACCGCGCGCGAGACCTACATTTAGGCTTACGAGCATATGAAAC 3360
QY      1561  CCGGACCTTCCCGTGTGCAAGACCATTTTGAATTTTGGAGGGGTCTTTACGGGTCT 1620
DB      3361  CCGGACCTTCCCGTGTGCAAGACCATTTTGAATTTTGGAGGGGTCTTTACGGGTCT 3420
QY      1621  ACCCATATGACGCGCATCTCTATCCAGACAAAGAGAGTGGGAAAACTTCCCTAT 1680
DB      3421  ACTCATATATGATGCCCATCTTTTATCCAGACAAAGAGTGGGAAAACTTCCCTAT 3480
QY      1681  CTGTAGGTATCAAGACACCGTGTGCTGTAGAGCTCAAGCCCTTCCCGTGTGGAG 1740
DB      3481  CTGTAGGTATCAAGACACCGTGTGCTGTAGAGCTCAAGCCCTTCCCGTGTGGAG 3540
QY      1741  CAGATGTGAAGTGTGTATCTGTGTCAAGCCCATCTTCATGTGGCAACACTCTGTCT 1800
DB      3541  CAGATGTGAAGTGTGTATCTGTGTCAAGCCCATCTTCATGTGGCAACACTCTGTCT 3600
```


| Accession | Sequence | Length |
|-----------|---|--------|
| Oy | 1801 TATGACCTGGGCGCGTCTTCACAAATGAAGTACACCTGAGGCAACCGACATCAACAATATATC | 1860 |
| Db | 3601 TACGAGCTAGGGCGCGCTGTTCAAGAAATGAATCAACCTGAGGCAACCAATCAACAAATATACATC | 3660 |
| Oy | 1861 ATGACATGATATGTCCGCTGACCTGGAGGTGCTCAACGAGTACCTGGAGTCTCGTTGGCGGC | 1920 |
| Db | 3661 ATGACATGCAATGTGGCGCGACCTGGAGGTGCTCAACGAGCACCTGGAGTCTCGTTGGCGGC | 3720 |
| Oy | 1921 GTTCTGGGCTGCTTTGGCGCGTATTTGCTATTCACAGGCTGCGTGGTATATGTAAGTAAAG | 1980 |
| Db | 3721 GTCTCGGTGCTCTGGCGCGGTATTTGCTGTCAACAGGCTGCGTGGTATATGTAAGTAAAG | 3780 |
| Oy | 1981 ATTGCTCTGTCCGGAAGACCCGCAATCATTAACCGACAGGGAAGTCTTACCCGGAGTTTC | 2040 |
| Db | 3781 ATCGCTTTGTCCGGGAAGACCCGCAATTATTACTGACGGAGAGTTCTTACCAAGAGTTTC | 3840 |
| Oy | 2041 GATGAATGAAAGAGTCTT | 2059 |
| Db | 3841 GATGAGATGAAGAGTCTT | 3859 |

RESULT 4
US-10-509-921-3

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? Sequence 3 Application US/10509921
? Publication No. US20050250093A1
? GENERAL INFORMATION:
? APPLICANT: SmithKline Beecham Corporation
? TITLE OF INVENTION: Hepatitis C Virus Sub-Genomic Replicons
? FILE REFERENCE: P51335
? CURRENT APPLICATION NUMBER: US/10/509,921
? CURRENT FILING DATE: 2004-10-01
? PRIOR APPLICATION NUMBER: 60/369,685
? PRIOR FILING DATE: 2002-04-03
? NUMBER OF SEQ ID NOS: 54
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 3
? LENGTH: 7992
? TYPE: DNA
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Thepolynucleotide sequence encodes sequences from
? US-10-509-921-3 HCV H77 (BB7-F1/P2) Replicons

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| | | | | |
|----------------------------|-------|-----------------|-----------|--------------|
| Query Match | 83.8% | Score 1727.8; | DB 7; | Length 7992; |
| Best Local Similarity | 89.9% | Pred. No. 0; | | |
| Matches 1852; Conservative | 0; | Mismatches 207; | Indels 0; | Gaps 0; |

| | | | |
|----|------|--|------|
| Qy | 1 | TTGGGGCTTATCAAGGCTTATGCCAGAGACAAAGGGGCTTTTGGATGTGATATACCC | 60 |
| Db | 1801 | ATGGGGCTTATTAACGGCTTACTCTCCMAAGACGCCAGGCTTACTGGCTGATATCACT | 1860 |
| Qy | 61 | AGCTTGACCGGCGGGGACAAAACCAAGGTGAGGGGTGAGTTTCAGATCGTGCATCTCT | 120 |
| Db | 1861 | AGCTTCACAGGCGGGGACAGAACCAAGTCCAGGGGGAGTTCAGATGCTTCCACGGCA | 1920 |
| Qy | 121 | GCCGACCTTTCTTGGCAACTGCATTTAAAGGGGTGTTGSACTGTCTACATGAGACC | 180 |
| Db | 1921 | ACAGATCTTTCCTGGCAGCTGGGCTCAATGGCGGTGTGTGACGTCTTATCATGTGGCC | 1980 |
| Qy | 181 | GGACACAGGACCATTTGCGTCACTTAAGGCTCTGTATTACAGATGTACACCAATGTGAC | 240 |
| Db | 1981 | GGCTCAAAAGACCTTGGCCGGGCTCAAAAGGGCCCAATCACCAATGTACCAAAATGTGAC | 2040 |
| Qy | 241 | CAAGACCTCTAGGGCTGGCGCGCTCCCAAGGTGCGCGCTCATTTAAACCAATGACCTTGC | 300 |
| Db | 2041 | CAGAGCTTTGTGGGCTGGCGCGCTCTTCAAGGTTTCGCCCTATATGACACCTGTACTGTC | 2100 |
| Qy | 301 | GGCTCTCTGGACCTTTACCTGGTCAACAGGACACGCCAATGTCATCTCTGTGCGCGACGG | 360 |
| Db | 2101 | GGCTCTCTGGACCTTTTACTGCTACAGAGGACACGCCAATGTCATCTCTGTCGCGCGGCA | 2160 |
| Qy | 361 | GGTAGAGGAGGAGCGCTGCTTTTCGCCCGGCTTATCTCTTACTTGAAGGCTCTCG | 420 |

| | | | |
|----|------|---|------|
| Db | 2161 | GGTAGATGACAGGGGTAGCTTCCTTTGGCCCCGGCCCATTTCTTACTTGAAAGGCTCTCG | 2220 |
| QY | 421 | GGAGGCCCTCTGCTGTGTGCCCCGACAGACATGCGGTAGGACATATTCAAGACCGCGTATGC | 480 |
| Db | 2221 | GGGGGTCCCGTGTGTGTGCCCCGGGGACACGCGTGGGCTTATTCAGGGCCGGGTGTGC | 2280 |
| QY | 481 | ACCGGTGAGTGGCTAAGGCGGTGGACTTCAATCCCCGTAGAGAGCTTAGAGACAACTATG | 540 |
| Db | 2281 | ACCGGTGAGTGGCTAAGGCGGTGGACTTCAATCCCCGTAGAGAGCTTAGAGACAACTATG | 2340 |
| QY | 541 | AGGTCCCCGGGTGTTCTGACAACTCCGCCACACAGAGGCCCCAGAGCTACCAAGTG | 600 |
| Db | 2341 | AGATCCCCGGGTGTTCTGACAGAACTCTTCTCACAGAGAGTCCCCAGAGCTTCAAGTG | 2400 |
| QY | 601 | GCCCACTGCATGTCTCCACCGGACGGGTAAAGACACAAAGTCCGGCCGACATACGA | 660 |
| Db | 2401 | GCCCACTGCATGTCTCCACCGGACGGGTAAAGACACAAAGTCCGGCGGTACGATACGA | 2460 |
| QY | 661 | GCTACGGGCTTACAAAGTGTGTGTCTCAACCCCTCGTGTCTGACAACTATGGCTTTGT | 720 |
| Db | 2461 | GCCCAAGGGCTTCAAGTGTGTGTCTCAACCCCTGTGTGTGACAAAGCTGTGGCTTTGT | 2520 |
| QY | 721 | GCTTACATGTCCAAAGGCCCATGGGATTTGATCTCTTAACATACAGACTGGGGGTAGGACATT | 780 |
| Db | 2521 | GCTTACATGTCCAAAGGCCCATGGGATTTGATCTTAATACAGAGCCGGGGGTAGAACATT | 2580 |
| QY | 781 | ACTATGCGACACCCGATCATCGTATTCCACCTACGGCAAGTTCTTTGCGACGGCGGTGT | 840 |
| Db | 2581 | ACCAATGGCAGCCCCATACGTACTCCACCTACGGCAAGTTCTTTGCGACGGCGGTGT | 2640 |
| QY | 841 | TCAGGGGGTGTATTGACATATAATTTGTGACAGATGCCATCTCACGGATGCACATCC | 900 |
| Db | 2641 | TCAGGAGGTGCTTATGACATATAATTTGTGACAGATGCCATCTCACGGATGCACATCC | 2700 |
| QY | 901 | ATCTTTGGGCAATTGGCATCTGTCTTTGACCAACAGACAGACCGGGGGGAGACTGACTGTG | 960 |
| Db | 2701 | ATCTTTGGGCAATCGGCATCTGTCTTTGACCAACAGACAGACCTGGGGGAGACTGACTGTG | 2760 |
| QY | 961 | CTGCGCACGCTACCCCTCGGGGCTCGTCACTGTGCCCACTCCATTCCTAACATGAGAGAGTT | 1020 |
| Db | 2761 | CTGCGCACGCTACCCCTCGGGGCTCGTCACTGTGTCCACTGTGTCCACTGACATGAGAGAGTT | 2820 |
| QY | 1021 | GCTCTGTCCACTACCGAGAGATCCCTTTTATGGAAGAGCTATTTCCCTTGAAGCAATT | 1080 |
| Db | 2821 | GCTCTGTCCACACCGAGAGATCCCTTTTATGGAAGAGCTATTTCCCTTGAAGAGATC | 2880 |
| QY | 1081 | AAAGGGGGGAGACATCTCATTTTCTGCCACTCAAAAGAAAGATGCGAGAGCTGGCGCA | 1140 |
| Db | 2881 | AAAGGGGGGAGACATCTCATTTTCTGCCACTCAAAAGAAAGATGCGAGAGCTGGCGCG | 2940 |
| QY | 1141 | AAACGTGTGCGGTGTGGGGGTCAAAAGCGGTGGCTTACTACCGGGGCTTGAATGTGCGGT | 1200 |
| Db | 2941 | AAAGCTGTGCGATTTGGGATCAAAAGCGGTGGCTTACTACCGGGGCTTGAATGTGTCTC | 3000 |
| QY | 1201 | ATCCGACCAAGTGTGACGTTGTGTGTGTGCAACTGACGCGCTCATGACCGGCTTTAC | 1260 |
| Db | 3001 | ATCCGACCAACGGGGAGTGTGTGTGTGTGTGACCGATGTCTCATGACGCGCTTTAC | 3060 |
| QY | 1261 | GGCGCACTTTCGATGTGTGTGTGACTGCAACAGTGTGTCTCATGACAGCTGATTTTCGC | 3120 |
| Db | 3061 | GGCGCACTTTCGATGTGTGTGTGACTGCAACAGTGTGTCTCATGACAGCTGATTTTCGC | 3120 |
| QY | 1321 | CTTGAACCTTACTTCAACATTTGAGCAATACGCGTCCCCAGAGATGCTGTCTCCGCT | 1380 |
| Db | 3121 | CTTGAACCTTACTTTCATTGAGCAACACGCTCCCCAGAGATGCTGTCTTCAAGACT | 3180 |
| QY | 1381 | CAAGCTCGGGGTAGGACTGACAGAGGAAAGCCAGGACATTACAGATTTGTGTGACACGGGG | 1440 |
| Db | 3181 | CAAGCTCGGGGCAAGACTGACAGAGGAAAGCCAGGACATTATAGATTTGTGTGACACGGGG | 3240 |
| QY | 1441 | GAGCGTCTTTGGGATTTTGAATCGTGTGTCTCTGCGAGTGTATGACGCGGCTTGT | 1500 |

Db 3241 GAGCGCCCTCCGCGATGTCAGTCTGCTCTGTGAGTGTAGACGGGGCTGT 3300
Qy 1501 GCTTGGTATGACCTTAACGGCCCGGAGACCAAGTTAGGCTACGACATATGAACACC 1560
Db 3301 GCTTGGTATGACCTCAACGGCCCGGAGACCAAGTTAGGCTACGACATATGAACACC 3360
Qy 1561 CCGGGACTCCCGTGTGCGCAAGACATCTGAAATTTTGGAGGGGCTTTTACGGGCTTC 1620
Db 3361 CCGGGGCTTCCCGTGTGCGCAAGACATCTGAAATTTTGGAGGGGCTTTTACGGGCTTC 3420
Qy 1621 ACCCATATGACGCCCATCTTCTATCCAGACAAAGCAGAGTGGGAAAACTTCTCTAT 1680
Db 3421 ACTCATATGATGACCCACTTTTATCCAGACAAAGCAGAGTGGGAGAACTTTCTCTTAC 3480
Qy 1681 CTGGTATGCTTACCAAGCCACCGTGTGCGTACAGAGTCAAGCCCCCTCCCGTGTGGAC 1740
Db 3481 CTGGTATGCTTACCAAGCCACCGTGTGCGTACAGAGTCAAGCCCCCTCCCGTGTGGAC 3540
Qy 1741 CAGATGTGGAAGTCTGTATCCGCTCAAGCCCACTTCATGGGCAACCTCTGTCTA 1800
Db 3541 CAGATGTGGAAGTCTGTATCCGCTTAAACCACTTCATGGGCAACCTCTGTCTA 3600
Qy 1801 TATAGACTGGCGCTGTCTCAGATGAAATCACTTGAACGACCACTCACTCAATATATC 1860
Db 3601 TACAGACTGGCGCTGTCTCAGATGAAATCACTTGAACGACCACTCACTCAATATATC 3660
Qy 1861 ATGACATGATGTGGCTGACCTGAGAGTGTCTACAGATGACTGGGTCTCGTTGGCGGC 1920
Db 3661 ATGACATGATGTGGCTGACCTGAGAGTGTCTACAGATGACTGGGTCTCGTTGGCGGC 3720
Qy 1921 GTTCTGTGCTTTGGCCGCGATTTGCTATCCACAGGCTGCGTCAATGATGATGAG 1980
Db 3721 GTTCTGTGCTTTGGCCGCGATTTGCTATCCACAGGCTGCGTCAATGATGATGAG 3780
Qy 1981 ATGTCTGTGCTTTGGAAAAAGCGCAATCAATCCCGACAGGAAATCTTACCGGAGTTC 2040
Db 3781 ATGTCTGTGCTTTGGAAAAAGCGCAATCAATCCCGACAGGAAATCTTACCGGAGTTC 3840
Qy 2041 GATGAATGGAAGATGCT 2059
Db 3841 GATGAATGGAAGATGCT 3859

RESULT 5
US-11-173-792-7
; Sequence 7, Application US/11173792
; Publication No. US20060019245A1
; GENERAL INFORMATION:
; APPLICANT: Rice III, Charles
; APPLICANT: Blight, Kerl
; TITLE OF INVENTION: HCV Variants
; FILE REFERENCE: 6029-4356
; CURRENT APPLICATION NUMBER: US/11/173,792
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US/09/576,989
; PRIOR FILING DATE: 2000-05-23
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 7
; LENGTH: 7848
; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-11-173-792-7

Query Match 67.0%; Score 1381.2; DB 8; Length 7848;
Best Local Similarity 79.4%; Pred. No. 0;
Matches 1635; Conservative 0; Mismatches 423; Indels 0; Gaps 0;

Qy 1 ATGGCGCCCTATACAGCCCTTATGCGCCGACGACAGCAAGGGGCTTTTGGAGTGCATATACCC 60
Db 1801 ATGGCGCCCTATATACAGCCCTTATGCGCCGACGACGCGAGGCTTATGCGTGCATATACCT 1860
Qy 61 ACCTGATCCGCGCGGACAAACCAAGTGAAGGTGAGGTTCAATCTGTCAACTGCT 120

Db 1861 AGCTCAAGGCGCGGACAGAGACCAAGGTCAGAGGGGAGGTCAAGTGTCTCCACCGCA 1920
Qy 121 GCCCAGACTTTCTTGGCACTGCTATTAACGGGGTGTGTTGAGCTGTCTACATGAGGCC 180
Db 1921 ACACATCTTTCTCGGCACTGCTCATATGAGCGGTGTGAGACTGTCTATCATGTGTGC 1980
Qy 191 GGAACAGAGACCATTTGGCTCACTAAGGGTCTGTATCCAGATGATACCAATGTGAC 240
Db 1981 GGTCAAGAACCTTTGCGCGCCCAAGGCGCCCAATCACTCAATATGACCAATGTGAC 2040
Qy 241 CAAGACTGTAGAGCTGCGCCGCTCCCAAGGTGCGCTCATTAACACATGACCTTGC 300
Db 2041 CAGAGCTGTGTGCGTGAAGCGCCCGCGGGGCGGTCTTGAACACATGACCTGCG 2100
Qy 301 GGTCTCTGAGACTTTACCTGTGTACAGAGGACCGCGATGTCTGTGTGCGCGACGG 360
Db 2101 GGCAGCTCGGACCTTTACTTGTGTCAAGAGGATGCGATGTCTATTCGGGTGCGCGCG 2160
Qy 361 GGTGATGGCAGGGGAGCGTGTTCGCGCGGCTATCTTACTTGAAGGCTCTCG 420
Db 2161 GGCAGACAGGGGAGGCTTACTTCTCCCAAGCCCGTCTCTACTTGAAGGCTCTTGC 2220
Qy 421 GGAGGCGCTTGTGTGCGCGCAGAGCATGCGCTAGGCAATATGAGACCGCGTATGC 480
Db 2221 GCGCGTCACTGTCTGCGCCCTCGGGGACAGCTGTGGGCAATCTTTCGGGCTGCGGTGTC 2280
Qy 481 ACCGTGAGATGTGCTAAGCGGTGAGCTTCACTCCCGTGAAGAGCTTGAAGACCAATG 540
Db 2281 ACCCGAGGGGTGTGCMAAGCGGTGAGCTTGTGACCGGTGAGTGAAGAACCACTATG 2340
Qy 541 AGGTCCCGGGTGTGTGAGACAACTCTCCACAGAGGTGCCAGAGTCAACCAAGT 600
Db 2341 CGGTCCCGGTCTTACGAGCAACTGTCTCTCCGCGGTACCGACATTTCCAGGTG 2400
Qy 601 GCCCATGCTGATGCTCCACCGGCAAGGTGAAGACCAAGTCCCGCGCATATGCA 660
Db 2401 GCCCATGCTGATGCTCCACCGGCAAGGTGAAGACCAAGTCCCGCGCATATGCA 2460
Qy 661 GCTCAGGGCTACAGGTGTGTGCTCAACCTCTCGTTGCTGCAACATGGGCTTTGCT 720
Db 2461 GCCCAAGGGTATTAAGTGTCTGTCTGTGAACCGGTGCGCGCACCTTAAAGTTCGGG 2520
Qy 721 GCTTACATGCTCAAGGCCCATAGGATGATCTTACATCAGGACTGGGGTGAAGCAAT 780
Db 2521 GCTTATATGTCTTAAGGCAATGTATGCACTTACATCAGAACCGGGTAAAGACATC 2580
Qy 781 ACTATGCGAGCCGATCAGATATTCACCTTACGCGCAAGTTCCTTCCGACGCGGTGT 840
Db 2581 ACCAAGGGTGGCCCATCACTGATCTCACTCACTTGAAGTTCCTTCCGACGCGGTGTG 2640
Qy 841 TCAGGGGTGCTTATGACATATTAATTTGTGACAGGTGCACTCCAGGATCAACATTC 900
Db 2641 TCTGGGGGCGCTTATGACATATTAATTTGTGAGTGTGCACTCACTCACTGACACT 2700
Qy 901 ATCTTGGGCAATTTGACATGCTCTTGAACCAAGGAGACCGCGGGGCGAGACTGACTG 960
Db 2701 ATCTTGGGCAATTTGACATGCTCTTGAACCAAGGAGACCGCTGAGCGCGACTGCTG 2760
Qy 961 CTGCGCACCGTACCCCTCCGGGCTCCGTCACTGTGCCCCATCTTACATCAGAGAGTT 1020
Db 2761 CTGCGCACCGTACCGCTCCGGGATCGGTCACTGCGCACCGTCACTCAATCAGAGAG 2820
Qy 1021 GCTCTGTCACTACCGGAGAGATCCCTTTTATGCGAAGGCTATTCCTTAAACATTT 1080
Db 2821 GCTCTGTCACTACCGGAGAGATCCCTTTTATGCGAAGGCTATTCCTTAAACATTT 2880
Qy 1081 AAGGGGGGAGACATCATCTTCTGCACTCAAGAAAGAGTGGAGGAGGCTCGCGCA 1140
Db 2881 AAGGGGGGAGACATCATTTTCTGCACTTCAAGAAAGAGTGGAGGAGGCTCGCGCG 2940
Qy 1141 AAATGTGTGCGGTGGGCTCAATGCGGTGCTTCACTCCGCGGCTTGAATGTCTGCTC 1200

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Db 2941 AAGGTCCGGCCTCGSACTCAATGCTGTAGCATATTAACGGGGCCTTGATGATCCGTC 3000
Qy 1201 ATCCGACCAAGTGTGACGTTTCTGTCGCACTGACGCCCTCATGACGGCTTTAC 1260
Db 3001 ATACCAACTGAGCGGAGACCTCATTTGTCGAGCAACGGAGCTCTAATGACGGGCTTTTAC 3060
Qy 1261 GCGGACTTCGATTCGGTGTATGACTGCAACAGTGTGTACACCCAGACAGTCCGACTTACG 1320
Db 3061 GCGGATTCGACTGACTGATGATGCACTGCAATATCATGTGTACCCAGACAGTCCGACTTACG 3120
Qy 1321 CTGACCCCTTACCTTCACTTGAAGACAGACCGTGCACAAGACGGCGGTGTACGCTCG 3180
Db 3121 CTGACCCCTTACCTTCACTTGAAGACAGACCGTGCACAAGACGGCGGTGTACGCTCG 3180
Qy 1381 CAACGTCCGGGGTGAAGCTGGGCAAGGAAACCAAGCATTAAGATTTGTGGACCGGG 1440
Db 3181 CAGCGGCGGAGGAGGCTGTGAGGGGAGAGATGGGATTTAAGTTTGTGACTCCAGGA 3240
Qy 1441 GAGCGTCTTCTGACGTTTGTGACTGTCTGTCTCTGCGAGTGTATGACGGGGTTGT 1500
Db 3241 GAACGGCCCTCGGGCATGTTGATTCCTGCTTCTGTGTGTGAGTGTATGACGGGGCTGT 3300
Qy 1501 GCTTGATGAGCTTACCGCCCGCGAGACACAGTTAGGCTACGAGCATATGAACACC 1560
Db 3301 GCTTGATGAGCTTACCGCCCGCGAGACCTCAGTTAGGTTGCGGGCTTACCTAAACACA 3360
Qy 1561 CCGGACCTTCCGCTGTGCGCAACCATCTTGAATTTTGGAGGGGCTTTTACGGGTCTC 1620
Db 3361 CCGGAGTTGCGCGTGTGCGCAACCATCTGAGATCTGGGAGAGGCTTTTACAGGCCCTC 3420
Qy 1621 ACCCATATGAGCGCCCACTTCTCTATCCAGACAAAGAGAGAGGAGAAACCTTCCCTAT 1680
Db 3421 ACCCATATGAGCGCCCACTTCTCTATCCAGACAAAGAGAGAGGAGAAACCTTCCCTAT 3480
Qy 1681 CTGAGTGGCTACCAAGCCACCGTGTGCGCTAGAGCTCAGCCCTCCCGTGTGGAGAC 1740
Db 3481 CTGAGTGGCTACCAAGCTACCGTGTGCGCTAGAGCTCAGCCCTCCCGTGTGGAGAC 3540
Qy 1741 CAGATGTGGAAGTGTGATCCGCTGTCAAGGCCCACTTCATGAGGCGCAACACTTGTCTA 1800
Db 3541 CAAATGTGGAAGTGTCTCATAGGGCTTAAAGCTTACGCTGACAGGGCGCAACGCCCTGTCTG 3600
Qy 1801 TATAGACTGGGCGCTGTCCAGATGAGTACACCTGACGACCCCAATCCCAAGTATATTC 1860
Db 3601 TATAGACTGGGCGCTGTCCAGATGAGTACACCTGACGACCCCAATCCCAAGTATATTC 3660
Qy 1861 ATGACATGATGTGCGCTGACCTGAGAGTGTCTACAGAGTACCTGGGTGTCTGTTGCGGAC 1920
Db 3661 ATGACATGATGTGCGCTGACCTGAGAGTGTCTACAGAGTACCTGGGTGTCTGTTGCGGAC 3720
Qy 1921 GTTCTGGCTGTGTTGGCGCGCTGATTTGCTTATCAAGAGTGTGCTGTATGATGAGTACG 1980
Db 3721 GTTCTGGCTGTGTTGGCGCGCTGATTTGCTTATCAAGAGTGTGCTGTATGATGAGTACG 3780
Qy 1981 ATGTCTTGTCCGGAAGCGCGGCAATCATACCGGACAGGAGAGTCCCTTACCGGGAGTTC 2040
Db 3781 ATCATCTTGTCCGGAAGCGCGGCAATCATACCGGAGAGTCTTTTACCGGGAGTTC 3840
Qy 2041 GATGAATGGAAGAGTGC 2058
Db 3841 GATGAATGGAAGAGTGC 3858

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RESULT 6
US-10-509-921-9
; Sequence 9, Application US/1050921
; Publication No. US20050250093A1
; GENERAL INFORMATION:
; APPLICANT: SmithKline Beecham Corporation
; TITLE OF INVENTION: Hepatitis C Virus Sub-Genomic Replicons
; FILE REFERENCE: P51335
; CURRENT APPLICATION NUMBER: US/10/509,921
; CURRENT FILING DATE: 2004-10-01

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; PRIOR APPLICATION NUMBER: 60/369,685
; PRIOR FILING DATE: 2002-04-03
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 7979
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The poly-nucleotide sequence encodes sequences from
; US-10-509-921-9

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Query Match      67.0% Score 1381.2; DB 7; Length 7979;
Beet Local Similarity 79.4%; Pred No. 0;
Matches 1635; Conservative 0; Mismatches 423; Indels 0; Gaps 0;

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Qy 1 ATGGCGCCTATCACGGCCTTATGCCAGACAGACAAAGGGCCTTTGGATGATGAATCAACC 60
Db 1801 ATGGCGCCTATTAACGGCCTTACTCCACAGACAGAGGCTTACTTGGTGCATCATCACT 1860
Qy 61 AGCTTGACCGGCGCGGACAAACCAAGTGAAGGTGAGGTTCAATCGTGTCAACTGCT 120
Db 1861 AGCTTGACAGGCGCGGACAGAACCAAGTGAAGGTGAGGTTCAATCGTGTCAACTGCT 1920
Qy 121 GCCGACCTTTCTTGGCAACCTGATTAACGGGGTGTGTGGACGTCTTACCATGAGGCC 180
Db 1921 ACACATCTTCTCTGCGACCTGCGTCAATGAGCGTGTGTGATGATGCTATCATGAGTGC 1980
Qy 181 GGAAACAGGACCATTTGCGTCACTTAAGGAGTCTGTATTCAGATGTACACCAATGTGAC 240
Db 1981 GGCCTAAGAACCTTTGCGGCGCCCAAGAGGCCCAATCAACCAATGTACCAATGTGAC 2040
Qy 241 CAAGACTGTGAGTGGCGCGCTCCCAAGGTGCCCTATTAACACCATGCACTTGC 300
Db 2041 CAGGACTGTGAGTGGCGCGCGCTCCCAAGAGGCCCAATCAACCAATGTACCAATGTGAC 2100
Qy 301 GGCCTGTGAGCTTTACCTGTGCAAGAGGCAAGCGGATGATTCGTGTGGCGGACGG 360
Db 2101 GGCAGCTGTGAGCTTTACCTGTGCAAGAGGCAAGCGGATGATTCGTGTGGCGGACGG 2160
Qy 361 GGTGATGAGGAGGAGCGAGCTGTCTTGTGCGCGCGCTTATCTTACTTGAAGAGCTCTTCG 420
Db 2161 GGCAGACAGGAGGAGGAGCTTACTTCTCCGAGGCCGCTCTTACTTGAAGGCTCTTCG 2220
Qy 421 GAGGCGCTTCTGTGTGCGCGCAGAGACATGCGGTAGAGCATTTAGAGCCGCGTATGC 480
Db 2221 GGCAGTCACTGTCTGTGCGCGCTGAGGAGACGCTGTGAGCATTTTCTGAGCTGCCGTGTC 2280
Qy 481 ACCCGTGAAGTGTGCAAGCGGTGAGCTTCAATCCCGGTAGAGAGCTTGAAGCAACCAT 540
Db 2281 ACCCGTGAAGTGTGCAAGCGGTGAGCTTGTGAACCGGTGAGTGTGAAGCAACCAT 2340
Qy 541 AGGTCCCGGTTGTCTAGACAACTCTCCACAGAGTGCAGGAGTCCCGAGTACCAAGTGC 600
Db 2341 CGGTCCCGGTTGTCTAGACAACTCTCTCCCGAGAGTGCAGGAGTCCCGAGTACCAAGTGC 2400
Qy 601 GCCCATCTGATGCTCCACCGGAGCGGTAAAGACACCAAGGTCCCGGCGCATACGCA 660
Db 2401 GCCCATCTAACGCGCCCTACTGTGAGCGGAAAGACACTAAGGTCCCGGCTGATACGCA 2460
Qy 661 GGTCAAGGCTAACAGGTGTGTGTCTCAACCCCTCCGTTGCTGCAACAAATGGGCTTTGT 720
Db 2461 GCCCAAGGCTAACAGGTGTGTGTCTCAACCCCTCCGTTGCTGCAACAAATGGGCTTTGT 2520
Qy 721 GCTTACATGTCCAAAGGCCCATGAGATTTACTTCAATCAGAGCTGGGGTGAAGCAATT 780
Db 2521 GGTATATGTCTTAAGGACATGTGTATCGACCTTACATCAAGAACGGGGTAAAGACATTC 2580
Qy 781 ACTATGCGAGCCGATCACTGATTTCACTTACGAGCAAGTTCTTGGCGGACGGCGGTGT 840
Db 2581 ACCAGGGGTGCCCATCACTGATTTCACTTACGAGCAAGTTCTTGGCGGACGGCGGTGTGC 2640

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| | | | |
|----|------|---|------|
| QY | 841 | TCAGGGGTCGTTATGACATATAATTTGTCACAGAGCCCTCCACGGATGCAACATCC | 900 |
| Db | 2641 | TCGCGGGGCGCTATGACATCATATAATGATAGTGCACCTCACTGATCCGACACT | 2700 |
| QY | 901 | ATCTTGGGCATTTGGCATCTGCTCTTGGACCAAGACAGAGCCGGGGGGCGACACTGATCTGTG | 960 |
| Db | 2701 | ATCTCTGGGCATTCGGCACAGTCTCTGACCAAGCGAGAGCGCTGGAGCGCACTGTCGTG | 2760 |
| QY | 961 | CTCGGCACCGTACCCCTCCGGGGCTCGGTCACTGTGCCCATCTTAACATTCGAGAGGTT | 1020 |
| Db | 2761 | CTCGGCACCGCTACGCGCTCCGGGATCGGTCAACGGGCCACATCCAAACATCGAGAGGTTG | 2820 |
| QY | 1021 | GCTCTGTCCACTACCGGAGAGATCCCCCTTTATGCGAAGGCTATTTCCCTTGAAGCAATT | 1080 |
| Db | 2821 | GCTCTGTCCACACTCGAGAGAAATCCCCCTTTATGGCAAAAGCATTCCTCCATCGAACATC | 2880 |
| QY | 1081 | AAGGGGGGAGACATCTCATCTTCTGCGCACTCAAGAAAGATGCGACAGACTCGCGCA | 1140 |
| Db | 2881 | AAGGGGGGAGAGCACTCATTTTCTGCAATTCAGAGAGAAATGTGATGAGCTGCCGCG | 2940 |
| QY | 1141 | AAACTGTGTGCGGTTGGCGGTCAATGCGTGGCTTAATAACGCGGCTTGTATGTGTCCGTC | 1200 |
| Db | 2941 | AAGCTGTGCGGCGCTCGACCTCAATGCTGTAGCATATTACCGGGGCTTGTATGTATCCGTC | 3000 |
| QY | 1201 | ATCCGCACCATGTGTGATGAGTGTGCTGTGGCACTGACGCCCTCATATGACCGGCTTTACC | 1260 |
| Db | 3001 | ATACCAATTAACGGAGAGTCAATGTCTATCAACGAGCGGTCTTAATGACGGGCTTTAAC | 3060 |
| QY | 1261 | GGCGCACTTCGATTCGGGTATGACTGCAACAGTGTGCACCCGACCAAGTGAAGCTTGAC | 1320 |
| Db | 3061 | GGCGATTTGCACTCAGTATGACTGCAATATATGTGTCAACCCGACAGTGAAGCTTGAC | 3120 |
| QY | 1321 | CTTGCACCTTACCTTCAACATTGAGCAATCAAGCTTCCCGAGATGCTGTCTCCGTAAT | 1380 |
| Db | 3121 | CTGCACCCGACCTTCAACATTGAGCAAGCAACCGTGCCAAAGCGGGTGTCAAGCTCG | 3180 |
| QY | 1381 | CAAGTCGGGGGTAGACTGCGCAGAGAGGAGCCAGGACTCTACAGATTTGTGTGACCGGG | 1440 |
| Db | 3181 | CAGCGGCAGGACAGACTGTGATAGGGGCGAGATGGCAATTTACAGTTTGTATCTTCAGGA | 3240 |
| QY | 1441 | GAGCGTCTTCTMGAGATGTTTGAATCGATGTCCTGTGCGAGTGTATGACGGCGGGTGT | 1500 |
| Db | 3241 | GACGCGCCCTCGGGCATTTTGATTTCTTCGCTTCTGTGCGAGTGTATGACGCGGGCTGT | 3300 |
| QY | 1501 | GCTTGTATGAGCTTACGCGCGCGAGACCAAGTTAGGCTTACGACATACATGAACACC | 1560 |
| Db | 3301 | GCTTGTATGAGCTCAAGCTCAGCGCGCGAGACCTCAAGTTAGGCTTACCTAAACACA | 3360 |
| QY | 1561 | CCGGGACTTCCCGTGTGCCAAGACCATTTTGAATTTTGGAGGGGCTTTTACGGGTCTC | 1620 |
| Db | 3361 | CCAGGGTTGCCCGTCTGCGCAGGACCATCTGAGAGTTCTGGGAGAGGTCCTTTTACAGGCTTC | 3420 |
| QY | 1621 | ACCCACATAGACGCCCATCTTCCTAATCCGAGCAAAAGCAGATGGGGAAAACCTTCCCTAT | 1680 |
| Db | 3421 | ACCCACATAGACGCCCATTTTCTTGTCTCCAGACTAGCAGGAGAGACAACTTCCCTTAC | 3480 |
| QY | 1681 | CTGTAGCGCTACCAAGCCAGCGTGTGCGCTAGAGCTCAAGCCCTTCCCGCTGTGGGAC | 1740 |
| Db | 3481 | CTGTAGCATACAGGCTTACGAGTGTGGCGCAGGGGCTCAAGGCTCAACCTCATCGTGGGAC | 3540 |
| QY | 1741 | CAGATGTGAAGTGTCTTATCCGTCTCAAGCCACCTTCAATGGGCCAAACCTCTGTCTA | 1800 |
| Db | 3541 | CAAAATGTGAAGTGTCTATACGCGCTTAAAGCTTACGCTGCAACGGGCCAAACCCCTGTCTG | 3600 |
| QY | 1801 | TATGACATGGGCGCTGTCCAGAAATGAATCAACCTCGAGGCAACCAAGTACCAAGTATATC | 1860 |
| Db | 3601 | TATAGGCTGGAGCGGCTTCAAAACGAGGTATCTACACAACCCCATTAACAAATATCATTC | 3660 |
| QY | 1861 | ATGACATATATGTCCGCTGACCTCGAGGTCGTCACGATTAACCTTGGGTCCTCGTTGGCGGC | 1920 |
| Db | 3661 | ATGCGATCATATGTCCGCTGACCTGGAAGTCTGTGACAGACACTGGGTGTCTGTATGGCGGA | 3720 |
| QY | 1921 | GTTCTGGCTGCTTTGGCGCGGTAATTCCTATTCACAGGCTGCGTGTGTCATGATGAGTAGG | 1980 |

| Accession | Sequence | Position |
|-----------|--|----------|
| Db | 3721 GTCTTAGCAGCTCTGCGCCGCGTATTGCTGACAAACAGGCGAGCTGATTTGTGGCAGG | 3780 |
| Qy | 1981 ATTGCTCTTGTCCGGAAGCCGGCAATCATACCCGACAGGGAAGTCTCTACCGGGAATTG | 2040 |
| Db | 3781 ATCATCTTTGTCGGGAAGCCGGCCATCATTTCCGACAGGGAAGTCTTTACCGGGAATTG | 3840 |
| Qy | 2041 GATGAATGGAAGAGTGC | 2058 |
| Db | 3841 GATGAGATGGAAGAGTGC | 3858 |

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RESULT 7
US-10-509-921-10
; Sequence 10, Application US/10509921
; Publication No. US20050250093A1
; GENERAL INFORMATION:
; APPLICANT: SmithKline Beecham Corporation
; TITLE OP INVENTION: Hepatitis C Virus Sub-Genomic Replicons
; FILE REFERENCE: P51335
; CURRENT APPLICATION NUMBER: US/10/509,921
; CURRENT FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: 60/369,685
; PRIOR FILING DATE: 2002-04-03
; NUMBER OF SEQ. ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 7979
; TYPE: DNA
; ORGANISM: Artificial Sequence
FEATURE:
; OTHER INFORMATION: Thepolynucleotide sequence encodes sequences from
US-10-509-921-10

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| | | | | |
|----------------------------|--------|-----------------|-----------|--------------|
| Query Match | 67.0% | Score 1381.2; | DB 7; | Length 7979; |
| Best Local Similarity | 79.4%; | Pred. No. 0; | | |
| Matches 1635; Conservative | 0; | Mismatches 423; | Indels 0; | Gaps 0 |

| | | | |
|----|------|---|------|
| QY | 1 | ATGCGCGCTTATCAGGCGCTTATGCCAGACAGCAAGGGGCGCTTTGGATGATATATACCC | 60 |
| Db | 1801 | ATGCGCGCTTATTAAGGCGCTTACTCCCAACAGCGAGGCGCTTACTTGGCTGATATACACT | 1860 |
| QY | 61 | AGCTTGAACCGGCGGGGCAAAAACCAAGTGGAGGGTGAAGTTTCAGATCGTCAACTGCT | 120 |
| Db | 1861 | AGCTTCAACGGCGGGGACAGAAACCAAGTCAAGGGGGAGTTCAAAGTGTCTCCACGGCA | 1920 |
| QY | 121 | GCCAGACTTTCCTTGGCACTGCAATTAACGGGGTGTGTGGACTGTCTACCATGAGCC | 180 |
| Db | 1921 | ACAACAATCTTTCCTGGGAGACTCGGTCATAGGCGTGTGTGGACTGTCTATCATGATGCC | 1980 |
| QY | 181 | GGAAACAAGAACATATGGCGTCAACCTTAAGGGTCTGTATCCAGATGTACCAATATGAGAC | 240 |
| Db | 1981 | GGCTCAAAAGACCTTTCGGCGGCCCAAAAGGCGCCAAATCACCAAAATGTACCAATATGAGAC | 2040 |
| QY | 241 | CAAGACTCTGAGGCTGGCGCGCTCCCAAGAGTCCCGCTCATTTAACAACCATGCACTTGC | 300 |
| Db | 2041 | CAGAGACTCTGTCGGCTGGCAAGGCGCGCCCGGGGGGGTTCCTTGACCAATGACCTGCG | 2100 |
| QY | 301 | GGCTTCCTGGACCTTTTACCTGTGTACAGAGGACGCGCATGTCAATTCCTGTGCGCCGACGG | 360 |
| Db | 2101 | GGCAGCTCGGACCTTTTACTGTGTACAGAGGACATCCCATGTCAATTCGGGTGCGCGGGGG | 2160 |
| QY | 361 | GGTATGCGCAGGGGACGCGCTTTCGGCGCGGCGCTTATCTTTACTTGAAGGCGCTCGG | 420 |
| Db | 2161 | GGCGACAGCAGGGGAGAGCTTACTTCTCCCAAGCGCGCGTCTCTCTTGAAGGCGCTCTTGG | 2220 |
| QY | 421 | GGAGGCGCTCTGTGTGTGCGCCCGACAGACATGCGCTAGGCAATTTCAAGCGCGCGGTATGC | 480 |
| Db | 2221 | GGCGGTCAACGTCTGTGCGCGCTCGGGGACGCTGTGGGCAATCTTTCGGGCTGCGCGTGGCG | 2280 |
| QY | 481 | ACCGGTGAGTGTGCTTAAGCGGTGTGACTTATCCCGTGAAGACTTATGAGACACATG | 540 |

Db 2281 ACCGAGGGGTTGCGAAGCGGTGACCTTTGTACCCGTGACGTATGAGAAACCACTATG 2340
 QY AGGTCCCGGTTTCTCAGACAACTCCCTCCCAACGAGTCCCAAGCTACCAAGT 600
 Db 541 AGGTCCCGGTTTCTCAGACAACTCCCTCCCAACGAGTCCCAAGCTACCAAGT 600
 Db 2341 CGGTCCCGGTTTCTCAGACAACTCCCTCCCAACGAGTCCCAAGCTACCAAGT 2400
 QY 601 GCCCACTGATGCTCCCAACGAGTCCCAAGCTACCAAGTCCCAAGCTACCAAGT 660
 Db 2401 GCCCACTGATGCTCCCAACGAGTCCCAAGCTACCAAGTCCCAAGCTACCAAGT 2460
 QY 661 GCTCAGGGGTACAGAGTGTGTGTCAACCCCTCCGTGTCGCAACATGAGGCTTTGT 720
 Db 2461 GCCCAAGGGGTATAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2520
 QY 721 GCTTACATGTCCAAAGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 780
 Db 2521 GGTATATGTCTAAGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2580
 QY 781 ACTACCTGAGGCTCCGATCTGATTCACCTACGAGGATTTCTTGTCCGACGAGGATG 840
 Db 2581 ACCACGGGTGCTCCGATCTGATTCACCTACGAGGATTTCTTGTCCGACGAGGATG 2640
 QY 841 TCAGGGGGGTCTTATGACATAATTAATTTGTGACGAGTCCACTCCAGATGCAATCC 900
 Db 2641 TCTGGGGGGGCTTATGACATAATTAATTTGTGACGAGTCCACTCCAGATGCAATCC 2700
 QY 901 ATCTTGGGATTTGGCACTGTCTTGTGACCAAGAGACCGCGGGGCGAGATGACTGTG 960
 Db 2701 ATCTTGGGATTTGGCACTGTCTTGTGACCAAGAGACCGCGGGGCGAGATGACTGTG 2760
 QY 961 CTGCGACCGGCTACCCCTCCGGGCTCCGATCTGATGCGGCTTCTTACGAGGAGTT 1020
 Db 2761 CTGCGACCGGCTACCCCTCCGGGCTCCGATCTGATGCGGCTTCTTACGAGGAGTT 2820
 QY 1021 GCTCTGTCTACCTACCGAGAGATCCCTTTTATGCGAAGCTATTCCTTTGAGCAAT 1080
 Db 2821 GCTCTGTCTACCTACCGAGAGATCCCTTTTATGCGAAGCTATTCCTTTGAGCAAT 2880
 QY 1081 AAGGGGGGAGACATCTCATCTTCTGCGCATGAAAGAAAGTGGAGAGAGTCCCGCA 1140
 Db 2881 AAGGGGGGAGACATCTCATCTTCTGCGCATGAAAGAAAGTGGAGAGAGTCCCGCA 2940
 QY 1141 AAATCTGTGCGCTTGGGCGTCAATGCGGCTTCTTCTTACCGGCGCTTGTATGTCCTG 1200
 Db 2941 AAATCTGTGCGCTTGGGCGTCAATGCGGCTTCTTCTTACCGGCGCTTGTATGTCCTG 3000
 QY 1201 ATCCGACCACTGTGACGTTGTCTGTGTGCACTGACGCGCTTCAATGACCGGCTTTAC 1260
 Db 3001 ATCCGACCACTGTGACGTTGTCTGTGTGCACTGACGCGCTTCAATGACCGGCTTTAC 3060
 QY 1261 GCGGACTTGTGATTCGCTGATTAAGCTGCAACAGTGTGTGACCCGAGCACTTCAAGC 1320
 Db 3061 GCGGACTTGTGATTCGCTGATTAAGCTGCAACAGTGTGTGACCCGAGCACTTCAAGC 3120
 QY 1321 CTGACCCGACTTACCACTTGAAGCAATCAGGCTTCCGAGAGTGTCTCCGCTACT 1380
 Db 3121 CTGACCCGACTTACCACTTGAAGCAATCAGGCTTCCGAGAGTGTCTCCGCTACT 3180
 QY 1381 CAACGTCGGGGTGAAGCTGCGAGAGGAGCAAGGATCTTACAGATTTGTGACCGAGG 1440
 Db 3181 CAACGTCGGGGTGAAGCTGCGAGAGGAGCAAGGATCTTACAGATTTGTGACCGAGG 3240
 QY 1441 GAGGCTCTTCTGTGCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1500
 Db 3241 GAGGCTCTTCTGTGCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3300
 QY 1501 GCTTGTATGAGCTTACGCGCGCGAGACACAGTTAGGCTACGAGCATATGAACACC 1560
 Db 3301 GCTTGTATGAGCTTACGCGCGCGAGACACAGTTAGGCTACGAGCATATGAACACC 3360
 QY 1561 CCGGAGCTTCCGCTGTGCGAAGCACTTGTGAATTTGTGAGGCGCTTTTACCGAGCTTC 1620
 Db 3361 CCGGAGCTTCCGCTGTGCGAAGCACTTGTGAATTTGTGAGGCGCTTTTACCGAGCTTC 3420

QY 1621 ACCGACATAGAGCGCCCACTTCTATCCAGACAAAGAGAGTGGGAAAACCTTCCCTAT 1680
 Db 3421 ACCGACATAGAGCGCCCACTTCTTGTCCAGACTAAGCAGGAGAGCAACTTCCCTAC 3480
 QY 1681 CTGTAGGCTTACCAAGCAACCGTGTGCGCTAGAGCTCAAGCCCTTCCCGGTGTGGAC 1740
 Db 3481 CTGTAGGCTTACCAAGCAACCGTGTGCGCGAGGCTCAAGGCTTCCCGGTGTGGAC 3540
 QY 1741 CAGATGTGAAGTCTTGTATCCGTCTCAAGCCCACTTCCATGAGGCAACCTTGTCTA 1800
 Db 3541 CAAATGTGAAGTCTTGTATCCGTCTCAAGCCCACTTCCATGAGGCAACCTTGTCTG 3600
 QY 1801 TATAGAGGCGGCTGTCCAGATGAGTCAACCTTCAAGGACCGACCTGACCAAGTATATC 1860
 Db 3601 TATAGAGGCGGCTGTCCAGATGAGTCAACCTTCAAGGACCGACCTGACCAAGTATATC 3660
 QY 1861 ATGACATGATGTCCGCTGACCTGAGAGTGTGTCAAGATACCTGTGTGTGTGTGTG 1920
 Db 3661 ATGACATGATGTCCGCTGACCTGAGAGTGTGTGTCAAGATACCTGTGTGTGTGTG 3720
 QY 1921 GTTCTGCTGCTTTGGCGCGCTTATTCATCAAGGCTGCTGTGTGTGTGTGTGTGTG 1980
 Db 3721 GTTCTGCTGCTTTGGCGCGCTTATTCATCAAGGCTGCTGTGTGTGTGTGTGTGTG 3780
 QY 1981 ATTGTCTTGTCCGGAAGCGGCAATCAATCCGCAAGGGAAGTCTTACCGGAGTTTC 2040
 Db 3781 ATTCATCTTGTCCGGAAGCGGCAATCAATCCGCAAGGGAAGTCTTACCGGAGTTTC 3840
 QY 2041 GATGAATGGAAGAGTGC 2058
 Db 3841 GATGAATGGAAGAGTGC 3858

RESULT 8
 US-10-509-921-4
 ; Sequence 4, Application US/10509921
 ; Publication No. US20050250093A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SmithKline Beecham Corporation
 ; TITLE OF INVENTION: Hepatitis C Virus Sub-Genomic Replicons
 ; FILE REFERENCE: P51335
 ; CURRENT APPLICATION NUMBER: US/10/509,921
 ; PRIOR FILING DATE: 2004-10-01
 ; PRIOR APPLICATION NUMBER: 60/369,685
 ; NUMBER OF SEQ ID NOS: 54
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 7980
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: The polynucleotide sequence encodes sequences from
 ; US-10-509-921-4

Query Match 67.0%; Score 1381.2; DB 7; Length 7980;
 Best Local Similarity 79.4%; Pred. No. 0;
 Matches 1635; Conservative 0; Mismatches 423; Indels 0; Gaps 0;

QY 1 ATGGGCGCTATTCAGCGGCTATGCCCCAGACAGCAAGGCGCTTTTGGAGTATATCAC 60
 Db 1801 ATGGGCGCTATTCAGCGGCTATTCGCCAAGACAGCGAGGCTTATGGCTGCAATCACT 1860
 QY 61 AGCTTGACCGGCGGGAACAACAGGATGAGGAGTGTGAGTTCAGATGCTGTCAACTGCT 120
 Db 1861 AGCTTGACCGGCGGGAACAAGACAGGATGAGGAGTGTGAGTTCAGATGCTGTCAACCGA 1920
 QY 121 GCCAGACTTTCTTGGCAACTGCAATTAACGGGAGTGTGTGTGACTGTCTACATGAGGC 180
 Db 1921 ACACATCTTCTCTGGCAACTGCAATTAACGGGAGTGTGTGTGACTGTCTATCATGATGCC 1980

181 GGAACAAGACCATTCGCTCACTTAAGAGGCTCTGTATCCAGATGTACCAATGTGAC 240
1981 GGCTCAAGAACCTTGTCCGGGCCCCAAAGGGCCCAATACCAAAATGTACCAATGTGAC 2040
241 CAAGACTCTGTAGGTGAGGCTGAGGCTCCCAAGGTGCGGCTATTAACCATGTGAC 300
2041 CAGGACTCTGTAGGTGAGGCTGAGGCTCCCAAGGTGCGGCTATTAACCATGTGAC 2100
301 GGCTCTGAGGACTTAACTGTGACAGAGGCAAGGAGATGATTCCTGTGCGGCGGAG 360
2101 GGCAAGTCTGAGGACTTAACTGTGACAGAGGCAAGGAGATGATTCCTGTGCGGCGG 2160
361 GGTAATGAGGAGGAGGAGGCTTATGCTGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
2161 GGCAAGTCTGAGGACTTAACTGTGACAGAGGCAAGGAGATGATTCCTGTGCGGCGG 2220
421 GGAAGGCTCTGTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 480
2221 GGCGGCTCACTGTCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 2280
481 ACCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
2281 ACCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2340
541 AGGTCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 600
2341 GGCTCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2400
601 GGCAAGTCTGAGGACTTAACTGTGACAGAGGCAAGGAGATGATTCCTGTGCGGCG 660
2401 GGCAAGTCTGAGGACTTAACTGTGACAGAGGCAAGGAGATGATTCCTGTGCGGCG 2460
661 GGCAAGTCTGAGGACTTAACTGTGACAGAGGCAAGGAGATGATTCCTGTGCGGCG 720
2461 GGCAAGTCTGAGGACTTAACTGTGACAGAGGCAAGGAGATGATTCCTGTGCGGCG 2520
721 GGTAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
2521 GGTAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2580
781 ACTAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
2581 ACCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2640
841 ACCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900
2641 ACCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2700
901 ACCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 960
2701 ACCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2760
961 ACCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1020
2761 ACCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2820
1021 ACCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1080
2821 ACCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2880
1081 ACCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1140
2881 ACCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2940
1141 ACCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1200
2941 ACCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3000
1201 ACCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1260
3001 ACCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3060
1261 ACCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1320

3061 GGCGATTTTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3120
1321 CTGAGCCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTAC 1380
3121 CTGAGCCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTAC 3180
1381 CAAGCTCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1440
3181 CAAGCTCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3240
1441 GAGCGCTCTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1500
3241 GAGCGCTCTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3300
1501 GAGCGCTCTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1560
3301 GAGCGCTCTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3360
1561 GAGCGCTCTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3420
3361 GAGCGCTCTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3480
1621 ACCCATAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1680
3421 ACCCATAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3480
1681 GAGCGCTCTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1740
3481 GAGCGCTCTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3540
1741 GAGCGCTCTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1800
3541 GAGCGCTCTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3600
1801 GAGCGCTCTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1860
3601 GAGCGCTCTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3660
1861 GAGCGCTCTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1920
3661 GAGCGCTCTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3720
1921 GAGCGCTCTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1980
3721 GAGCGCTCTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3780
1981 GAGCGCTCTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2040
3781 GAGCGCTCTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3840
2041 GAGCGCTCTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2058
3841 GAGCGCTCTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3858

RESULT 9
US-10-509-921-5
; Sequence 5, Application US/1050921
; Publication No. US2005025093A1
; GENERAL INFORMATION:
; APPLICANT: SmithKline Beecham Corporation
; TITLE OF INVENTION: Hepatitis C Virus Sub-Genomic Replicons
; FILE REFERENCE: P51335
; CURRENT APPLICATION NUMBER: US/10/509,921
; PRIOR FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: 60/369,685
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 7980
; TYPE: DNA

ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Thepolynucleotide sequence encodes sequences from
OTHER INFORMATION: HCV H77 (BB7-F3(C)) Replicons
US-10-509-921-5

Query Match 67.0%; Score 1381.2; DB 7; Length 7980;
Best Local Similarity 79.4%; Pred. No. 0;
Matches 1635; Conservative 0; Mismatches 423; Indels 0; Gaps 0;

QY 1 ATGGCGCTATACGCGCTTATGCTCCAGCAGACAGAGCGCGCTTTTGAGATGATATACACC 60
DB 1801 ATGGCGCTATATACGCGCTTATGCTCCAGCAGACAGAGCGCTTATGAGATGATATACACC 1860
QY 61 AGCTTGACCGCGCGGAGCAAAAACAAGTGGAGGAGTGAAGTTCAGATGCTGCACTGCT 120
DB 1861 AGCTTGACAGCGCGGAGCAAAAACAAGTGGAGGAGTGAAGTTCAGATGCTGCTGCACTGCT 1920
QY 121 GCCCAGACTTTCTTGAGCAACCTGCAATTAACGGGGTGTGTGAGACTGTCTACAGTGAAGCC 180
DB 1921 ACACATCTTTCTGCTGCGACCTGCTCAATGCGCTGTGTGTGAGACTGTCTATATATGTGCTC 1980
QY 181 GGACACAGAGACCATTTGCTGCTACCTTAAGGCTCTGTTATTCAGATGTATACCAATGTGAGC 240
DB 1981 GGCTCAAGAGACCTTTGCTGCGGCGCCAAAGGGCCCAATCACCAATATGTATACCAATGTGAGC 2040
QY 241 CAAGACCTCTGTAGTGGCTGGCGCGCTCCCAAGTGGCGCTCATTTAACCAATGCACTTGC 300
DB 2041 CAGAGACTGTGCTGGCTGGAGAGCGCGCGCGCGCGCTTCTTGAACACAGTACGACTGTC 2100
QY 301 GGCCTCTGAGACCTTTACCTGTGTCAAGAGGACGCGAGTGTATTCCTGTGCGCGAGCG 360
DB 2101 GGCAGCTGAGACCTTTACCTGTGTCAAGAGGACGCGAGTGTATTCCTGTGCGCGAGCG 2160
QY 361 GGTGATGCGAGGGGAGCGCTGCTTTTGCGCGCGCTTATCTTACTTGAAGAGCTCTCG 420
DB 2161 GGCGACAGAGGGGAGCGCTTCTCTCCCGAGCGCGCTCTTACTTGAAGAGCTCTCG 2220
QY 421 GAGAGCCCTTGTGCTGTGCGCGAGAGACATGCGGTAGGACATTTAGAGCCCGGTATGC 480
DB 2221 GCGGCTGCACTGCTCTGCGCGCTGCGAGCGCTGTGGGACATTTTGGGCTGCGCTGTC 2280
QY 481 ACCCGTGAAGTGGCTTAAGGCGGTGAGCTTATCCCGGTAGAGAGCTTAGAGCAACATTC 540
DB 2281 ACCCGAGGGGTGCGAAGCGGTGAGCTTATCCCGGTAGAGAGCTTAGAGCAACATTC 2340
QY 541 AGGTCCCGGTGTGTCAAGACAACTCTCCCGACAGAGTCCCGAGAGTACCAAGTGC 600
DB 2341 CGGTCCCGGTCTTACCGGACAACTGCTCCCGCGGTACCGGAGCATTTCCAGGTG 2400
QY 601 GCCCAGCTGATGTCTCCACCGCGAGCGGTAAAGACCAAGGTCCCGCGCATACGCA 660
DB 2401 GCCCATCTACACGCGCTACTGTAGCGGCAAGAGACATTAAGTCCCGCTCCGATGCA 2460
QY 661 GGTGAGGCTAAGGTGTGTGCTCAACCCCTCGTTGCTGCAACATAGGAGCTTTGGT 720
DB 2461 GCCCAAGGTATTAAGGTGTGTGCTTGAACCCGCTCGTGCAGCACTTAGGTTTGGG 2520
QY 721 GCTTACATGTCCAGAGCCCATGAGTATGCTTAACATCAGAGACTGGGTGAGACAAT 780
DB 2521 GGTATATGTCTAAGGACATAGTATCGACCTTAACATCAGAAACGGGGTAAAGACATC 2580
QY 781 ACTTACTGCAAGCGCGATCAGATTTCACTTACAGGCAAGTTCCTTGGCGAGCGGGGT 840
DB 2581 ACCAGCGGGTCCCGCATCAGTATCTCACTTGAAGTATTTCTTGGCCACGCTGATGTC 2640
QY 841 TCAGGGGGGTCTTATGACATTAATATTGTGAGAGTGCACCTCAGCGAGCAATCC 900
DB 2641 TCTGGGGGGCTTATGACATTAATATTGTGAGAGTGCACCTCAGCTGACACT 2700
QY 901 ATCTTGGGATTTGGCACTGTCTCTTGAACAGAGAGACCGCGGGCGAGACTGACTGTG 960
DB 2701 ATCTTGGGATTTGGCACTGTCTCTTGAACAGAGAGACCGCTGAGCGGAGCTGCTGCTG 2760

QY 961 CTCGCCACGCTAACCCCTCCGGGCTCCGCTCACTGTGCCCCCATCTTAATCATGAGAGGT 1020
DB 2761 CTCGCCACGCTAACCCCTCCGGGATCGGTCAACCGGTCCCAATCAATCATGAGAGGT 2820
QY 1021 GCTCTGTCACTTACCGGAGAGATCCCTTTATAGCAAGCTATTTCCCTTGAAGCAAT 1080
DB 2821 GCTCTGTCACTTACCGGAGAGATCCCTTTATAGCAAGGATCCCATCATGAGAGATC 2880
QY 1081 AAGGGGGGAGACATCTATCTTCTGCGACATCAAGAAAGTGTGAAGAGTGGCGGCA 1140
DB 2881 AAGGGGGGAGACATCTATCTTCTGCGACATCAAGAAAGTGTGAAGAGTGGCGGCA 2940
QY 1141 AAATGTGTGCGGTTGGGCGTCAATGCGGTGCTTACTACCGCGCTTATGTGCTGCTC 1200
DB 2941 AAGCTGTGCGGCTTGGGCGTCAATGCGGTGCTTACTACCGCGCTTATGTGCTGCTC 3000
QY 1201 ATCCGACCAAGTGTGAGCTGTGTGCTGTGCGCACTGACGCGCTTATGACCGGCTTTAAC 1260
DB 3001 ATACCAACTAAGGAGAGAGCTGATGTGCTGAGCAAGAGCGCTTATGACCGGCTTTAAC 3060
QY 1261 GCGCACTTGTGATGTGTATGACTGCAACAGTGTGTACCCAGACAGTGTGACTTCAAC 1320
DB 3061 GCGCACTTGTGATGTGTATGACTGCAACAGTGTGTGTACCCAGACAGTGTGACTTCAAC 3120
QY 1321 CTGACCCCTACCTTACCATTTGAGCAATACAGCTTCCCGAGATGTGTCTCCGCTACT 1380
DB 3121 CTGACCCCTACCTTACCATTTGAGCAATACAGCTTCCCGAGATGTGTCTCCGCTACT 3180
QY 1381 CAACGTGCGGGTGTGAGCTGTGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1440
DB 3181 CAGCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3240
QY 1441 GAGGCTCTTGTGAGATGTGTATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1500
DB 3241 GAAAGGCTCTTGTGAGATGTGTATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3300
QY 1501 GCTTGTATGAGCTTACCGCGCGCGAGAGCAACAGTTAGGCTTACGAGCATATGAAACAC 1560
DB 3301 GCTTGTATGAGCTTACCGCGCGCGAGAGCAACAGTTAGGCTTACGAGCATATGAAACAC 3360
QY 1561 CCGGACTTCCCGTGTGCGAAGACCATCTTGAATTTTGGAGGAGGCTTTTACGGGCTTC 1620
DB 3361 CCGGAGTTCGCGGTGTGCGAAGACCATCTTGAATTTTGGAGGAGGCTTTTACGGGCTTC 3420
QY 1621 ACCCATATGAGCGCCCATCTTCTATCCAGACAAAGCAGAGTGGGAGAACTTCCCTAT 1680
DB 3421 ACCCATATGAGCGCCCATCTTCTATCCAGACAAAGCAGAGTGGGAGAACTTCCCTAT 3480
QY 1681 CTGTGAGGCTTACAGCCACCGTGTGAGCTTGAATTTTGGAGGAGGCTTTTACGGGCTTC 1740
DB 3481 CTGTGAGGCTTACAGCCACCGTGTGAGCTTGAATTTTGGAGGAGGCTTTTACGGGCTTC 3540
QY 1741 CAGATGTGAAGTGTGTATCCGCTCAAGCCCATCTTCAATGAGGCAACCTCTGTCTA 1800
DB 3541 CAGATGTGAAGTGTGTATCCGCTCAAGCCCATCTTCAATGAGGCAACCTCTGTCTA 3600
QY 1801 TATAGCTGGGAGCGGTTCAAAACGAGGTTACTACCAACACCCCATTAACCAATATATC 1860
DB 3601 TATAGCTGGGAGCGGTTCAAAACGAGGTTACTACCAACACCCCATTAACCAATATATC 3660
QY 1861 ATGATATATGTGCGGTGAGCTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTG 1920
DB 3661 ATGATATATGTGCGGTGAGCTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTG 3720
QY 1921 GTTCTGTGCTTGTGGCGCGCTATGCTTATCCAGGCTGTGCTGTATATAGTATAG 1980
DB 3721 GTTCTGTGCTTGTGGCGCGCTATGCTTATCCAGGCTGTGCTGTATATAGTATAG 3780
QY 1981 ATTGTCTGTGCGGAAAGCGGCAATCATACCGACAGGAAAGTCTCTACCGGAGTTC 2040
DB 3781 ATTCATCTGTGCGGAAAGCGGCAATCATACCGACAGGAAAGTCTCTTACCGGAGTTC 3840

QY 2041 GATGAATGAGAGTGC 2058
| | | | |
Db 3841 GATGAGATGAGAGTGC 3858

RESULT 10
US-11-173-792-5
; Sequence 5, Application US/11/173792
; Publication No. US20060019245A1
; GENERAL INFORMATION:
; APPLICANT: Rice III, Charles
; APPLICANT: Blight, Keril
; TITLE OF INVENTION: HCV Variants
; FILE REFERENCE: 6029-4356
; CURRENT APPLICATION NUMBER: US/11/173,792
; CURRENT PILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US/09/576,989
; PRIOR FILING DATE: 2000-05-23
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 7987
; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-11-173-792-5

Query Match 67.0%; Score 1381.2; DB 8; Length 7987;
Best Local Similarity 79.4%; Pred. No. 0;
Matches 1635; Conservative 0; Mismatches 423; Indels 0; Gaps 0;

QY 1 ATGGGCGCTATACAGGCGCTATGCGGAGCAGACAGAGGCGCTTTTGAGATGATTAATCAC 60
| | | | |
Db 1801 ATGGGCGCTATTAACGGCTTAATCCAGACAGAGGCGCTTAATGCTGATCACTACT 1860

QY 61 AGCTTGACCGCGCGGAGCAAAAACAGGTGAGGGTGAAGTTCAGATCGTCAACTGCT 120
| | | | |
Db 1861 AGCTTCACAGCGCGGAGCAGAAACAGGTGAGGGGAGGTCAAGTGTCTCCACCGCA 1920

QY 121 GCCGACCTTTCTTGCGCAACCTTGACCTTAACGGGGTGTGTGACGTGTCAATGAGAGCC 180
| | | | |
Db 1921 AACAAATCTTCTTGCGACGCTGCAATGAGCGTGTGTGAGCTGTCTATCATGATGTC 1980

QY 181 GGAAGAGGACCATTTGCGCTACCTAAGGCTCTGTTATCCAGATGATACCAATGTGAC 240
| | | | |
Db 1981 GGCTCAAAAGCCTTGTGCGGCGCCAAAGGCCCAATACCAATATGATACCAATGTGAC 2040

QY 241 CAAGAATCTGTAGGTGCGCGCTGCCCTCCAAAGTGCCTCATTAACCATGACTTGC 300
| | | | |
Db 2041 CAGGACCTGTGCGGTGCGCAGCGCGCCCGGGGCGCTTCTTGACACATGCACTGC 2100

QY 301 GGCTCTGAGACCTTAACCTGATCAAGAGCAGCGGATGATTCCTGTGCGCGAGCG 360
| | | | |
Db 2101 GGAGCTCGAGACCTTAACCTGATCAAGAGCAGCGGATGATTCCTGTGCGCGAGCG 2160

QY 361 GGTGATGAGGAGGAGAGCTGCTTTCGCGCGGCTATCTTAACTTTGAAAGCTCTTCG 420
| | | | |
Db 2161 GGCGAGAGAGGAGGAGAGCTTCTCCCGCAAGCCCGTCTCTTAATGAGGGCTCTTCG 2220

QY 421 GAGAGCGCTCTGCTGTGCGCGGAGAGCATGCGGTGAGGATTAACAGAGCGCGTATGC 480
| | | | |
Db 2221 GGCGGTGCACTGCTGTGCGCGGTGAGCGGTGAGGATCTTTCGCGGTCTCCGTGTGC 2280

QY 481 ACCCGTGAAGTGGCTTAAGCGGAGTGAATTCATCCCGTGAAGAGCTTGAAGCAACATG 540
| | | | |
Db 2281 ACCCGAGGGGTGAGAGGCGGTGAGCTTTGTAACCGGTGAGTCTAATGAAACCACTAG 2340

QY 541 AGGTCCCGGCTTCTCAGACAACTCTCCCGACAGAGTGCAGGAGTCCCGGAGTCAAGAG 600
| | | | |
Db 2341 CGGTCCCGGCTTCTCAGAGCAACTGTCTCCCGGAGGAGTGCAGGAGCAATTCAGAGTG 2400

QY 601 GCCCATCTGATGCTCCAGCGGAGCGGTGAAGAGCAACAGGTCCCGGCGCATACGA 660
| | | | |
Db 2401 GCCCATCTGATGCGCGCTCTAGTGTAGCGGAGAGAGCATTAAGTGTCCGGCTCGTATGCA 2460

QY 661 GCTCAGGGCTAACAGGTGCTGTGCTCAACCCCTCGTTGCTGCAACATGAGGCTTTGGT 720
| | | | |
Db 2461 GCCCAAGGTATTAAGTGTCTGTCTGAACCCGTCGCGCCACCTAGAGTTTCGGG 2520

QY 721 GCTTACATGTCCAGAGCCCATGGAATGATCTTAACATCAGAGCTGGGGTGAAGCAATT 780
| | | | |
Db 2521 GGTATATGTCTAAGAGCAGATGTATCGACCTTAACATCAGAAACGGGGTAAAGACATTC 2580

QY 781 ACTACTGACCGCGATACGATATTCCACTAAGCGCAAGTTCCTTGCGGACGGCGGTCT 840
| | | | |
Db 2581 ACCAGGGTGGCCCATACGATACCACTAATGAGCAAGTTCCTTGCGGACGGGTGTGC 2640

QY 841 TCAGGGGTGCTTATGACATATAATTGTGACAGTGTGCACTCCAGGATCAACATCC 900
| | | | |
Db 2641 TCTGGGGGCGCTATGACATCATATATGTATGATGTGCTCACTCAATGATCTGACACT 2700

QY 901 ATCTTGGGCAATYGGCACTGTCTTTGACCAAGCAGAGCCGGGGGAGACTGACTGTG 960
| | | | |
Db 2701 ATCTGGGCAATCGGACAGTCTGTGACCAAGCGAGAGCGGTGAGCGGACTGTGCTG 2760

QY 961 CTGCGCACCGCTACCCCTCGGGGCTCGCTCACTGTGCCCCATCTTAATCAGAGAGTT 1020
| | | | |
Db 2761 CTGCGCACCGCTACCGCTCGGGATCGGTCAACCGGCAATCCAAACATCAGAGAGGTG 2820

QY 1021 GCTCTGTCCACTACCGGAGAGATCCCTTTATGCGAAGGCTATTCCCTTGAACAAATT 1080
| | | | |
Db 2821 GCTCTGTCCAGACTGAGAAATCCCTTTATGCGAAGGCTATTCCCATGAGACATC 2880

QY 1081 AAGGGGGGAGACATCTCATCTTCTGCCACTCAAGAAAGAGTGGCAGAGCTGCGCGCA 1140
| | | | |
Db 2881 AAGGGGGGAGACATCTCATTTTCTGCCATTCCAAAGAAATGATGAGTCTGCCGCG 2940

QY 1141 AAATGTGTGCGGTGGGCTCAATGCCGTGCTTAACCGGGCTTGATGTGCTGCTG 1200
| | | | |
Db 2941 AAGGTGTGCGGCTCGACTCAATGTGTGATGATTAACCGGGCTTGATGTGCTGCTG 3000

QY 1201 ATCCGACCAATGTGAGCTGTGCTGTGCGTGGCACTGACGCGCTCATGACCGGCTTTACC 1260
| | | | |
Db 3001 ATACCAATGACGAGAGCTCATTTGTCTGACGAGACGCTCTTAATGAGCGGCTTTACC 3060

QY 1261 GGCGACTTTCATTTGCGGTATGACTGCAACAGCTGTGTCAACAGAGTGCATTTCAAC 1320
| | | | |
Db 3061 GGCGATTTTCATCTGATGATGCAATGATGATGTGTCAACAGAGTGCATTTCAAC 3120

QY 1321 CTGACCTTACCTTACCATTTGAGACATCAACGCTTCCCGAGAGTGTCTTCCGTAAT 1380
| | | | |
Db 3121 CTGACCTTACCTTACCATTTGAGACATCAACGCTTCCCGAGAGTGTCTTCCGTAAT 3180

QY 1381 CAAGCTCGGGTAAAGACTGCGAGAGAGGAGCAAGGATCTTACAGATTTGTGCAACGGGG 1440
| | | | |
Db 3181 CAGCGGCAAGGAGAGCTGTGAGGGGAGAGATGGGCAATTTACAGGTTGTGCTCCAGGA 3240

QY 1441 GAGCGTCTTTCGCGATTTTGAATCTGTGTCTCTGCGAGTGTATGACGCGGGTGT 1500
| | | | |
Db 3241 GAAAGCGCTCTCGGGGATGTTGATCTCTCGGTTCTGTGAGTGTATGACGCGGGTGT 3300

QY 1501 GCTTGTATGAGCTTACCGCCCGCGAGACCAAGTTAAGCTTACGAGCATACATGAACCC 1560
| | | | |
Db 3301 GCTTGTATGAGCTTACCGCCCGCGAGACTTCAAGTTAAGTGTGCGGCTTACCTTAACCA 3360

QY 1561 CGGGACTTCCCGTGTGCGCAAGACCATCTTGAATTTTGGAGGGGCTTTTACGGGCTTC 1620
| | | | |
Db 3361 CGAGGTTGCGGCTGTGCGCAAGACCATCTTGAAGTTCTGGAGAGGCTCTTTTACAGGCTTC 3420

QY 1621 ACCCATATAGACGCCCATCTTCTATCCAGACAAAGCAGAGTGGGAAAACTTCTCTAT 1680
| | | | |
Db 3421 ACCCATATAGAGGCCCATTTCTTGTCCAGACTAAGCAGGAGGAGCAAACTTCTCTATC 3480

QY 1681 CTGTTAGGTATCAAGACCAACGCTGTGCGCTGAGGCTCAAGCCCTTCCCGTGTGGAGC 1740
| | | | |
Db 3481 CTGTTAGGTATCAAGGCTTACGCTGTGCGCAGGGGCTCAGGCTTCCACTTCATCTGTGGAGC 3540

Qy 1741 CAGATGTGGAAGTGTGATCCGTCTCAAGCCCACTTCATGAGCCAAACCTCTGCTA 1800
 Db 3541 CAAATGTGGAATGTCTCTATACGGCTTAAAGCTTACGCTGCAAGGCGCAAGCCCTGCTG 3600
 Qy 1801 TATAGACTGGGCGCTGTCCAGATGAATGACCTTGACGCGACCCAGTCAACAAATATATC 1860
 Db 3601 TATAGGCTGGAGCCGTTCAAAACAGAGTTACTACCAACACCCCAATAACAAATATATC 3660
 Qy 1861 ATGAATGATGATGCTGGCTGACCTTGAGAGTCTCAAGATGACCTGGGTGCTCTTGGCGGC 1920
 Db 3661 ATGGATGATGATGCTGGCTGACCTTGAGAGTCTCAAGATGACCTGGGTGCTCTTGGCGGC 3720
 Qy 1921 GTTCTGGCTGCTTGTGCGGCGCGATGATGCTATCCAGAGGCTGGGTGCTATGATGATG 1980
 Db 3721 GTTCTGAGAGCTCTGTGCGCGCGATGATGCTATCCAGAGGCTGGGTGCTATGATGATG 3780
 Qy 1981 ATGTCTGTGCTGGGAAAGCGGCAATCATACCGACAGGAAAGTCTTACCGGAGTTTC 2040
 Db 3781 ATCATCTGTGCTGGGAAAGCGGCAATCATACCGACAGGAAAGTCTTACCGGAGTTTC 3840
 Qy 2041 GATGAAATGGAAGAGTGC 2058
 Db 3841 GATGAAATGGAAGAGTGC 3858

RESULT 11
 US-11-173-792-8
 ; Sequence 8, Application US/11173792
 ; Publication No. US2006019245A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rice III, Charles
 ; APPLICANT: Blight, Kerl
 ; TITLE OF INVENTION: HCY Variants
 ; FILE REFERENCE: 6029-4356
 ; CURRENT APPLICATION NUMBER: US/11/173,792
 ; CURRENT FILING DATE: 2005-07-01
 ; PRIOR APPLICATION NUMBER: US/09/576,989
 ; NUMBER OF SEQ ID NOS: 21
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 8
 ; LENGTH: 7987
 ; TYPE: DNA
 ; ORGANISM: Hepatitis C virus
 US-11-173-792-8

Query Match 67.0%; Score 1381.2; DB 8; Length 7987;
 Best Local Similarity 79.4%; Pred. No. 0;
 Matches 1635; Conservative 0; Mismatches 423; Indels 0; Gaps 0;

Qy 1 ATGGCGCTTATCAAGGCTTATGCTTATGCAAGAGGCGCTTTTGGATGATTAATCACC 60
 Db 1801 ATGGCGCTTATCAAGGCTTATGCTTATGCAAGAGGCGCTTTTGGATGATTAATCACC 1860
 Qy 61 AGCTTACCGCGCGGGAAGAAACAGAGTGAAGGAGTTCAGATGCTGCACTGCT 120
 Db 1861 AGCTTACCGCGCGGGAAGAAACAGAGTGAAGGAGTTCAGATGCTGCACTGCT 1920
 Qy 121 GCCGACCTTCTTGCACACTGCAATTAAGGAGTGTGTTGATGCTGTACCATGAGGC 180
 Db 1921 ACACATCTTCTTGCACACTGCGCTGCAATGAGGTGTGTTGATGCTGTACCATGAGGC 1980
 Qy 181 GGAACAGAGCAATGCTGCTACCTTAAGGCTCTGTTATCCAGATGTAACCAATGTGAC 240
 Db 1981 GCTCAAGAGCAATGCTGCTGCTACCTTAAGGCTCTGTTATCCAGATGTAACCAATGTGAC 2040
 Qy 241 CAAGACCTGTAGGCTGCGCGCTCCCAAGAGTCCGCTCAATTAACCAATGACCTTGC 300
 Db 2041 CAAGACCTGTAGGCTGCGCGCTCCCAAGAGTCCGCTCAATTAACCAATGACCTTGC 2100
 Qy 301 GGCTCTGCGAGCTTATCTGTGTAAGAGGCAAGCGGATGCTATCTCTGTGCGCGAGCG 360
 Db 2101 GGCTCTGCGAGCTTATCTGTGTAAGAGGCAAGCGGATGCTATCTCTGTGCGCGAGCG 2160

Qy 361 GGTATGAGAGGAGGAGGCTGCTTTCGCGCGGCTTATCTTATCTTGAAGGCTCTGCG 420
 Db 2161 GGTATGAGAGGAGGAGGCTGCTTTCGCGCGGCTTATCTTATCTTGAAGGCTCTTTCG 2220
 Qy 421 GGAAGGCTCTGCTGCTGCGCGGAGAGATGCGGATGATTAAGAGCGCGGATGATG 480
 Db 2221 GGAAGGCTCTGCTGCTGCGCGGAGAGATGCGGATGATTAAGAGCGCGGATGATG 2280
 Qy 481 ACCGTGAGATGAGTGAAGCGGATGATTAAGAGCGCGGATGATTAAGAGCGCGGATG 540
 Db 2281 ACCGTGAGATGAGTGAAGCGGATGATTAAGAGCGCGGATGATTAAGAGCGCGGATG 2340
 Qy 541 AGGTCCCGGAGTGTCTGAGACAACTCTCCCAAGAGTCCCGAGAGTCCCGAGTACCAAGT 600
 Db 2341 AGGTCCCGGAGTGTCTGAGACAACTCTCCCAAGAGTCCCGAGAGTCCCGAGTACCAAGT 2400
 Qy 601 GCCCATCTGATGCTCCCAAGCGGATGATGAGACCAAGGTCGCGCGCATGACGA 660
 Db 2401 GCCCATCTGATGCTCCCAAGCGGATGATGAGACCAAGGTCGCGCGCATGATGACGA 2460
 Qy 661 GCTCAGGCTTACAGAGTGTGCTCAACCCCTCTGCTGCTGCAACATGAGGCTTTGAT 720
 Db 2461 GCTCAGGCTTACAGAGTGTGCTCAACCCCTCTGCTGCTGCAACATGAGGCTTTGAT 2520
 Qy 721 GCTTATGATGCTCAAGGCGCATGAGTGTGATCTTATCATGAGATGAGGAGTGAACAAT 780
 Db 2521 GCTTATGATGCTCAAGGCGCATGAGTGTGATCTTATCATGAGATGAGGAGTGAACAAT 2580
 Qy 781 ACTATGAGAGCGCGCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 840
 Db 2581 ACTATGAGAGCGCGCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2640
 Qy 841 TCAAGGAGGCTTATGATGATTAATTTGTGACAGTGTGCTTCAAGGATGCAACATTC 900
 Db 2641 TCAAGGAGGCTTATGATGATTAATTTGTGACAGTGTGCTTCAAGGATGCAACATTC 2700
 Qy 901 ATCTGGGATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 960
 Db 2701 ATCTGGGATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2760
 Qy 961 CTGCGCACCGTACCCCTCCGCGCTCCGCTCACTGTCGCCCATCTTAATCAGAGGAT 1020
 Db 2761 CTGCGCACCGTACCCCTCCGCGCTCCGCTCACTGTCGCCCATCTTAATCAGAGGAT 2820
 Qy 1021 GCTCTGTCCACTACCGAGAGATGCCCTTTATGAGCAAGGCTATTCCTTTAAGCAAT 1080
 Db 2821 GCTCTGTCCACTACCGAGAGATGCCCTTTATGAGCAAGGCTATTCCTTTAAGCAAT 2880
 Qy 1081 AAGGGGGGAGACATCTCATCTTCCGACCTCAAGAGAGAGTGGAGAGAGTCCCGCA 1140
 Db 2881 AAGGGGGGAGACATCTCATCTTCCGACCTCAAGAGAGAGTGGAGAGAGTCCCGCA 2940
 Qy 1141 AAACGTGTGCGCTTGGGCGTCAATGCGGCTTATCAAGGCGCTTATGATGATGATG 1200
 Db 2941 AAACGTGTGCGCTTGGGCGTCAATGCGGCTTATCAAGGCGCTTATGATGATGATG 3000
 Qy 1201 ATCCGACAGTGTGAGGCTGTGCTGCTGCACTGAGCGCTTATGACCGGCTTTTAC 1260
 Db 3001 ATCCGACAGTGTGAGGCTGTGCTGCTGCACTGAGCGCTTATGACCGGCTTTTAC 3060
 Qy 1261 GGGGACCTTGCATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
 Db 3061 GGGGACCTTGCATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 3120
 Qy 1321 CTGACCTTACCTTACCAATGAGCAATCAAGCTTCCCAAGAGTGTGCTCCGCTACT 1380
 Db 3121 CTGACCTTACCTTACCAATGAGCAATCAAGCTTCCCAAGAGTGTGCTCCGCTACT 3180
 Qy 1381 CAAGCTCGGAGTGAAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
 Db 3181 CAAGCTCGGAGTGAAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3240

| | | | |
|---|------|---|------|
| Qy | 1441 | GAGGCTCTTTCGGCATGTTGTAAGTCTGCTCTCTCTGCGAGTGTATGACGGGGTTGT | 1500 |
| Db | 3241 | GAACGGCCCTCGGGGATGTTGCAATTTCTCCGGTTCTGTGCGAGTGTATGACGGGGCTGT | 3300 |
| Qy | 1501 | GCTTGATGTAAGCTTAAGCGCCCGCGAGACCAAGTTAGGCTAACGAGCATACATGAACACC | 1560 |
| Db | 3301 | GCTTGATGTAAGCTTAAGCGCCCGCGAGACCTCAAGTTAGTTGCGGGCTTAACCTAAACACA | 3360 |
| Qy | 1561 | CCGGGACTTCCCGTGTGCGAAGACCATTGTGAATTTTGGAGGGCGTCTTTACGGAGCTC | 1620 |
| Db | 3361 | CCAGGGTGTCCCGCTGTCGACGAGACCATCTGGAGTTCTGGAGAGCGTCTTTACAGGCCTC | 3420 |
| Qy | 1621 | ACCCACATNAGACGCCCACTTCTCTATCCCAAGCAAAAGCAGATGGGGAACACTTCCCTAT | 1680 |
| Db | 3421 | ACCCACATNAGACGCCCACTTCTTGTCCCAACTAAGCAGGAGAGACAACTTCCCTTAC | 3480 |
| Qy | 1681 | CTGGTAGCGTACCAAGCACCCTGTGCGCTAGAGCTCAAGGCCCTCCCGCGTGGAGAC | 1740 |
| Db | 3481 | CTGGTAGCATACAGGCTACGGGTGTGCGCCAGGGCTCAAGGCTTCACTCTCCATCGTGGAC | 3540 |
| Qy | 1741 | CAGATGTGGAAGTCTGATCCGTCCTCAAGGCCACCCCTCATGGGCCCAACACTCTGCTA | 1800 |
| Db | 3541 | CAATGTGTGAAGTGTCTATACGGCTAAAGCTTAAGCTTAAGCTGACAGGGCCAAACGCCCTGCTG | 3600 |
| Qy | 1801 | TATATAGCTGGGCGCTGTCTCAGAAATGAAGTCAACCTGACAGCACCCAGTACCAATATATC | 1860 |
| Db | 3601 | TATATAGCTGGAGCCGTTCAAAACGAGGTATCTACACACACCCCATTAACCAATATACATC | 3660 |
| Qy | 1861 | ATGACATGTATGTGCGCTGACCTTGAGGTCGTCAACGAGTACCTGGGTGCTCGTTGGCGGC | 1920 |
| Db | 3661 | ATGGCATGTCAATGTGCGCTGACCTTGAAGGTCTGTACAGAGCACTGGGTGCTGTAGTGGCGA | 3720 |
| Qy | 1921 | GTTTCGCTGCTTTGGCGCGGTATTTGCTTATCCACAGGCTGCGTGTATATGATGATAGG | 1980 |
| Db | 3721 | GTCCTAGCAGCTCTGGCCGCGTATTTGCTGTACAAACAGGCAACGTCGTATTTGTGGGCAAGG | 3780 |
| Qy | 1981 | ATTGTCCTTGTCCGGAAGCCGCGCAATCATACCCGACAGGGAAAGTCTCTACGGGAGTTC | 2040 |
| Db | 3781 | ATCATCTTGTCCGGAAGCCGCGCATCATTTCCGACAGGAAATCTTTACCGGAGATTC | 3840 |
| Qy | 2041 | GATGAAATGGAAGATGC 2058 | |
| Db | 3841 | GATGAGATGGAAGATGC 3858 | |
| RESULT 12 | | | |
| US-11-173-792-13 | | | |
| : Sequence 13, Application US/1173792 | | | |
| : Publication No. US20060019245A1 | | | |
| GENERAL INFORMATION: | | | |
| : APPLICANT: Rice III, Charles | | | |
| : APPLICANT: Blight, Keril | | | |
| : TITLE OF INVENTION: HCV Variants | | | |
| : FILE REFERENCE: 6029-4356 | | | |
| : CURRENT APPLICATION NUMBER: US/11/173,792 | | | |
| : CURRENT FILING DATE: 2005-07-01 | | | |
| : PRIOR APPLICATION NUMBER: US/09/576,989 | | | |
| : PRIOR FILING DATE: 2000-05-23 | | | |
| : NUMBER OF SEQ ID NOS: 21 | | | |
| : SOFTWARE: PatentIn Ver. 2.0 | | | |
| : SEQ ID NO 13 | | | |
| : LENGTH: 7987 | | | |
| : TYPE: DNA | | | |
| : ORGANISM: Hepatitis C virus | | | |
| US-11-173-792-13 | | | |

| Query Match | Similarity | Score | 1381.2 | DB 8 | Length | 7987 | |
|-------------|------------|--|--------|------------|--------|--------|---|
| Best Local | 79.4% | Pred. No. 0 | | | | | |
| Matches | 1635 | Conservative | 0 | Mismatches | 423 | Indels | 0 |
| | | | | | | Gaps | 0 |
| Qy | 1 | ATGGGGCCTTATCAGCGCCTATGCCGACGACAAAGGGGCTTTTGGATGCATATACACC | 60 | | | | |
| Qb | 1801 | ATGGGGCCTTATCAGCGCCTACTCCCAAGACGACGAGCGCCTACTGGCTGCATATACACT | 1860 | | | | |

| | | | |
|----|------|--|------|
| OY | 61 | AGCTTAAACCGGCGGGGACAAAACACAGGTGAGAGGTGAGGTTCAAGTCTGTCACTGCT | 120 |
| Db | 1861 | AGCTTCACAGGCGCGGGACAGAAACCAAGTGCAGAGGGGAGGTCCAAAGTCTCCACCGCA | 1920 |
| OY | 121 | GCCGAGACTTTCCTTGGCACTTGATTAACGGGGGTGTGTGAACTGTCTCACTGAGACC | 180 |
| Db | 1921 | ACACAACTTTCCTGGGAGACTGTGTCAATGGGTGTGTGTGAACTGTCTCATGTGGGCC | 1980 |
| OY | 181 | GGAACAGAGAACATGTGCTCACTTAAGGTTCTGTATTCAGATGTACACCAATGTGAGC | 240 |
| Db | 1981 | GGCTCAAAAGACCTTGGCCGGCCAAAGGGCCCAATCACCAAAATGTACCAAAATGTGAGC | 2040 |
| OY | 241 | CAAAACCTCGTAGGCTGTGGCCCGCTCCCAAGGTGCCCGCTCAATTAACACATGACTTGC | 300 |
| Db | 2041 | CAGGAACTCGTGGCTGTGGCAAGGCCCCCGGGGGGGGTTCCTTGACACATGACACTGC | 2100 |
| OY | 301 | GGCTCTCGGACCTTTACTGTGTACAGAGGACGCGCATGTCAATCCTGTGCGCCGACG | 360 |
| Db | 2101 | GGCAGCTTCGACCTTTACTGTGTACAGAGGACATGCGATGTCAATTCGGTGGCGCGCG | 2160 |
| OY | 361 | GGTGATGGCAGAGGGAGAGCTGTGTCGCCCGCGCTATCTCTTAATTGAAAGGCTCTCG | 420 |
| Db | 2161 | GGCACAAGCAGGGGGAGACTCTCTCCCAAGCGCGCTTCCATACTTGAAGGGCTCTTCG | 2220 |
| OY | 421 | GGAGGCGCTGTGCTGTGTCCCGGAGGACATGCGGTAGGACATATTCAGAGCGCGGTATG | 480 |
| Db | 2221 | GGCGGTCCACTGTCTGTGTCCCTCGGGGACAGCTGTGGGACTCTTGGCGCTCGCTGTG | 2280 |
| OY | 481 | ACCCTGTAGTGTGCTAAGCGGTGAGACTTCACTCCGTTAGAGAGCTTAAAGACCACTG | 540 |
| Db | 2281 | ACCAGAGGGGTGTGGAAAGCGGTGACTTGTATCCCTCGAGCTTAGAGAAACCACTATG | 2340 |
| OY | 541 | AGGTCCCCGGGTTCCTAGACAACTCCTCCCAACAGCACTGGCCCCAGACTTCAAGTG | 600 |
| Db | 2341 | CGGTCCCCGGCTTTCACGAGCAACTGTCCCTTCGGCGGTACCGCAGACATTCAGGTG | 2400 |
| OY | 601 | GCCCACTGTGACTCTCCACCGGACGGGAGGTAAAGACCAAGGTCCGGCCGATACGA | 660 |
| Db | 2401 | GCCCATCTAACCGCCCCCTCACTGGTAGGCGGACAGAGCACTAAGGTGCCGCTGCTATGA | 2460 |
| OY | 661 | GCTCAGGGCTTAACAAAGTGTGTGTGTCTCAACCCCTCGGTGTCTGCACAAATGGGCTTGT | 720 |
| Db | 2461 | GCCCAAGGGTAATAGGTGTGTGTCTGTGAACCGGTCTGTGCGCCGACCTTAAGGTTCGG | 2520 |
| OY | 721 | GCTTACATGTGTCAAGGCGCCATGGATGTATCTTAACATCAAGACTGGGGGTGAGGACAATT | 780 |
| Db | 2521 | GGGTATATGTCTAAGGACATGTGTATGACCTCTTAACATCAAGAACGGGGGTAAAGCAATC | 2580 |
| OY | 781 | ACTACTGGACGCCGATCACTATTCACCTAAGGCAAGTTCTTGTCCAGCGCGGTGT | 840 |
| Db | 2581 | ACCACGGGTGCCCCCACTCACTCACTCACTTAAGGCMAAGTTTCTTGGCGAGGTGTGTG | 2640 |
| OY | 841 | TCAAGGGGGGTCTATGTACATTAATTTGTAGAGAGTGCACATCGATGTGCAATCC | 900 |
| Db | 2641 | TCTGGGGGCGCTATGTACATCATATATATGTATGTAGTGCACCTCAACTGTACACACT | 2700 |
| OY | 901 | ATCTTGGGCAATTGGCACTGTCTTGTACCAAGCAGAGACCGCGGGGCGAGACTGACTGTG | 960 |
| Db | 2701 | ATCTTGGGCAATCGGCAAGTCTGTGACCAAGCGGAGCGGCTGGAAGGCGACTCTGTGTG | 2760 |
| OY | 961 | CTGCGCACCGTACCCCTTCGGGGCTCGGTCACTGTGCCCATCTCTAACATTCAGAGAGTT | 1020 |
| Db | 2761 | CTTCCACCGGTACGCTTCGGGATCGGTACCGTGCACATCCAAACATTCAGAGAGGTG | 2820 |
| OY | 1021 | GCTTGTGTCACTACCGAGAGATCCCTTTTATGTGGCAAGGCTATTCCTCTTGAAGCAATT | 1080 |
| Db | 2821 | GCTTGTGTCAAGCACTGAGAAATCCCTTTTATGTGGCAAGCAATCCCATTCAGAGACATC | 2880 |
| OY | 1081 | AAGGGGGGAGACATCTCATCTTCTGTGCACTCAAAAGAAAGTGCAGAGCTTCGCCGCA | 1140 |
| Db | 2881 | AAGGGGGGAGAGCACTCATCTTCTGTGCACTTCCAAAGAAAGTATGTATGTGTGCTGCGCG | 2940 |

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Oy 1141 | AAACGTGCGGGTTCGGGCGTGAATGTCCTGGCTTACTACCGCGGCGCTTGAATGTCGCTC 1200
Db 2941 | AAGCTGTCGGGCGCTCGGACTCAATGCTGTATACATATTAACCGGGGCGCTTGAATGATCCGTC 3000
Oy 1201 | ATCCGACCAATGCGTGAAGTTCGTGCGTCGTGGCAACTGACGCGCTCATGACCGGCTTATACC 1260
Db 3001 | ATTACCACTACCGAGAGAGCTCATTTGTCTACCAACGACGCTCTAATGACGGGCTTATACC 3060
Oy 1261 | GGCGCATTTGCAATTCGGGTATGAGACTGCAACAGTGTGTCAACCCAGACAGTGCATTGAC 1320
Db 3061 | GGCGATTTGCACTCAGTATGATGCACTGCAATTCATGTGTCAACCCAGACAGTGCATTGACG 3120
Oy 1321 | CTTGACCTTACTCTTACCATTTGAGACATTCACGCTTCCCCAGAGTGTCTGTCTCCCGTACT 1380
Db 3121 | CTGGACCCGACCTTTCACCATTTGAGACGACGACCGTGCACAAAGCGGGTGTCAAGCTCG 3180
Oy 1381 | CAACGTCGGGGGTAGGACTGCGCAGAGGAGGAGGACAGGACATCTACATATTTGTGGCAGCGGG 1440
Db 3181 | CAGCGGCGAGGAGAGACTGTGTATGGGGGACAGATGGGCAATTTACAGATTTGTATCTCCAG 3240
Oy 1441 | GAGCGTCTCTTGCGCATGTTGACTCGTCTGTCTCTGCGAGTGTCTATGACGCGGGTGT 1500
Db 3241 | GAAAGGCGCTCGGGGATGTTGCAATTCCTCGGTTCTGTGCGAGTGTATGACGCGGGCGT 3300
Oy 1501 | GCTTGTGTATGAGCTTACGCGCGCGGAGACCAAGTATAGGCTTACGAGCATATGAAACAC 1560
Db 3301 | GCTTGTGTACGAGCTCACCGCGCGGAGACCTTCAGTATAGTGTGCGGGCTTACCTTAAACAC 3360
Oy 1561 | CCGGAGCTCCCGGTGTGCGCAAGACCATTTGAAATTTTGGGAGGGGCGTCTTACGGGCTC 1620
Db 3361 | CCAAGGTTGCCCGTCTGCGAGGACCATTTGAGATTCTGGGAGAGGTCCTTACAGGCTC 3420
Oy 1621 | ACCGACATAGACGCGCACCTTCTCTATCCCGACAAAGCAGATGGGAGAAAACCTTCCCTAT 1680
Db 3421 | ACCGACATAGACGCGCACTTCTGTCTGTCCAGACTAAGCAGGAGAGACAACTTCCCTAC 3480
Oy 1681 | CTGGTAGCGTACCAAGCCACCGTGTGCGCTTGAAGCTCAAGCCCTCCCCGTCGTGGAC 1740
Db 3481 | CTGGTAGCATACCAAGCTTACCGTGTGCGCCAGGGCTCAGGCTCCACCTCCGTCGGGAC 3540
Oy 1741 | CAGATGTGGAAGTGTCTGATCCGTGTCAAGGCCACCCCTCAATGGGCGCAACCTCTGCTA 1800
Db 3541 | CAATGTGGAAGTGTCTATACGGCTTAAGCCTTACGCTGCACGGGCGCAAGCCCTGCTG 3600
Oy 1801 | TATAGACTGGGCGCTGTCCAGATGAGTCAACCTGACGCAACCGCAGTCAACCAATATATC 1860
Db 3601 | TATAGGCTGGGAGCGCTTCAAAAGAGTTTCTACACACACCCCATATCAATATATC 3660
Oy 1861 | ATGACATGATGTGCGGCTGACCTGAGAGTGTCTCACAGTACTCTGAGTCTGTTGGCGGC 1920
Db 3661 | ATGGCATTCATGTGCGGCTGACCTGAGAGTGTCTCACAGTACTCTGAGTCTGTTGGCGGA 3720
Oy 1921 | GTTCTGGGCTGTTTGGCGCGGTATTTGCTTATCCACAGGTCGGTGTCTATGTATGTATAGG 1980
Db 3721 | GTCTCAGAGCTCTGGCGCGGTATTTGCTTACCAACAGGCAAGCGTGTCTATGTATGTATAGG 3780
Oy 1981 | ATGTGCTTGTCCGGAAGCCGGAATCATACCCGACAGGGAAGTCTCTACCGGGAATTC 2040
Db 3781 | ATCATCTTGTCCGGAAGCCGGAATCATCTTCCGACAGGGAAGTCTTTCACGGGAATTC 3840
Oy 2041 | GATGAAATGGAAGAGTGC 2058
Db 3841 | GATGAGATGGAAGAGTGC 3858

RESULT 13
US-10-509-921-6
; Sequence 6, Application US/10509921
; Publication No. US20050250093A1
; GENERAL INFORMATION:
; APPLICANT: SmithKline Beecham Corporation
; TITLE OF INVENTION: Hepatitis C Virus Sub-Genomic Replicons
; FILE REFERENCE: P51335

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| | | |
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| | CURRENT APPLICATION NUMBER: US/10/509,921 | |
| | PRIOR FILING DATE: 2004-10-01 | |
| | PRIOR APPLICATION NUMBER: 60/369,685 | |
| | PRIOR FILING DATE: 2002-04-03 | |
| | NUMBER OF SEQ ID NOS: 54 | |
| | SOFTWARE: FastSeq for Windows Version 4.0 | |
| | SEQ ID NO 6 | |
| | LENGTH: 7989 | |
| | TYPE: DNA | |
| | ORGANISM: Artificial Sequence | |
| | FEATURE: | |
| | OTHER INFORMATION: Thepolynucleotide sequence encodes sequences from | |
| | OTHER INFORMATION: HCV H77(HB7/H77NS5E)Replicons | |
| | US-10-509-921-6 | |
| Query Match | 67.0%; Score 1381.2; DB 7; Length 7989; | |
| Best Local Similarity | 79.4%; Pred. No. 0; | |
| Matches 1635; Conservative | 0; Mismatches 423; Indels 0; Gaps 0 | |
| Dy | 1 ATGCGCTTATCAGCGCTTATGCCAGACAGACAGGGCCCTTTGGATGCATTATCAC | 60 |
| Db | 1801 ATGGCGCTTATTCAGCGCTTACTCCAAAGACGCAAGCCCTTACTTGCGTCATCATCT | 1866 |
| Dy | 61 AGCTTGACCGCGCGGAGAAAACAAGGTGAAGGTGAGGTTCAGATGCTGCACTGCT | 120 |
| Db | 1861 AGCTTCACAGCGCGGAGAACCAAGTTCAGAGGGAGGTTCAGAGTGTTCACCGCA | 1922 |
| Dy | 121 GCCCAGACTTTCTTGGCAACTGCATTAAAGGGGTGTGTGGACTGTACCATTGAGCC | 180 |
| Db | 1921 ACACATCTTCTTGCGCACTGCGCTCAATGGCGTGTGTGGACTGTCTATCATGTGTC | 1988 |
| Dy | 181 GGACCAAGAACCATTTGCGTCACTTAAGGGTCTGTATTCAAGATGTAACCAATGTGAC | 240 |
| Db | 1981 GGCTCAAAGACCTTGGCCGCCCAAGGGCCCAATCAACCAATGTATGACCAATGTGAC | 2044 |
| Dy | 241 CAAGACTCTTAGGTGTGCGCGCTCCCAGAAGTGTGCGGCTCAATTAAACCATGCACTTCC | 300 |
| Db | 2041 CAGACCTCTGTGTGCTGACAGAGCGCCCCCGGGGGCGTCTCTTAACACCAAGCACTTGC | 2100 |
| Dy | 301 GGCTCTCTGGAACCTTTAATCTGGTCAAGAGGACGCGCATGTCTATCTGTGCGCGGACG | 360 |
| Db | 2101 GGCACTCGGACCTTTACTTGTGTCAAGGACATGCCATGTCTATCTCGGTGCGCGCGG | 2166 |
| Dy | 361 GGATGAGCAGGGGAGCGCTGTGCGCCCGGCTTATCTCTTAATTGAAGGCTCTCTG | 420 |
| Db | 2161 GGCGCAGACAGGGGGAGGCTTACTCTCCCAAGGCCGCTCTCTTAATTGAAGGCTCTTGC | 2222 |
| Dy | 421 GGAGGCTCTGTGTGTGCGCGCGGACAGACATGTCCGTAAGGCATTTCAAGGCCGCGTATGC | 480 |
| Db | 2221 GGCGGTCACTGTCTGTGCGCGCGGACAGCTGTGGGCACTTTTCGGGCTGCGGTGTC | 2288 |
| Dy | 481 ACCGTGAGTGGCTTAAGCGCGGTGACTTCACTCCCGTAGAGAGCTTTAGAGCAACATG | 540 |
| Db | 2281 ACCGAGGGGTTCGABAGCGGTGACTTTGTATCCCGTGTGAGTCTATGAGAACCACTATG | 2344 |
| Dy | 541 AGGTCCCGGTGTGTCTCAACAACCTCTCCCAACGAGAGTGCCTCCAGACTACCAAGTG | 600 |
| Db | 2341 CGGTCCCGGTCTTCAACGAGCAACTGTCTCCCTCGGCGGTATCCGCAATTTCCAGGTG | 2400 |
| Dy | 601 GCCCACTGACATGCTCCACCGGACGCGTAAAGACACCAAGSTCCCGGCGCATATGCA | 660 |
| Db | 2401 GCCCATCTTACACGCGCTTATGTATGCGGCAAGACACATAAGTGTCCGCTGCGATGCA | 2466 |
| Dy | 661 GCTCAGGCTTCAAGGTGTGTGCTCAACCCCTGCTGTGCAACAATGGGCTTTGGT | 720 |
| Db | 2461 GCCCAAGGATATAGGTGTGTGTCTTGAACCGGTCTGTGCTGCGCACCTTATGATTTGGG | 2522 |
| Dy | 721 GTTACATGTCCAGAGGCCATGGAATTGATCTTAACATCAGAGACTGGGTGAGCAATT | 780 |
| Db | 2521 GGATATATGTCTAAGGACATGTATGTACCTTAACATCAGAACCGGGGTAAAGCACTC | 2588 |
| Dy | 781 ACTACTGCAAGCCGATCACTATTTCACCTAAGGCAAGTTCTTGGCGAGCGGGGTGT | 840 |

Db 2581 ACCACGGGAGCCCCCATCACTACCTATGGAAGTTCTTGCGACGGTGGTGC 2640
Qy 841 TCAGGGGGGTGCTTATGACATATATTTGTGACAGTGGCACTCCACGGATGCAATCC 900
Db 2641 TCTGGGGGGGCTTATGACATATATTTGTGAGTGGCACTCACTGACCTGACCACT 2700
Qy 901 ATCTTGGGCACTGGCACTGCTCTTGAACCAAGAGAGACCGCGGGGCGAGACTGACTGTG 960
Db 2701 ATCTTGGGCACTGGCACTGCTCTTGAACCAAGAGAGACCGCTGAGACCGGACTGCTGTG 2760
Qy 961 CTGCGCACCGCTTACCTCTCGGGGCTTCCTGCTACTGTGCCCCATCTTAATCGAGAGGTT 1020
Db 2761 CTGCGCACCGCTTACCTCTCGGGGCTTCCTGCTACTGCGCCATCTCAAAATCGAGAGGTTG 2820
Qy 1021 GCTCTGTCCACTACCGGAGAGATCCCCCTTTATGCGAAGGCTATTCCTTTAAGCAATT 1080
Db 2821 GCTCTGTCCAGACTCGGAGAGAAATCCCCCTTTATGCGAAGGCTATTCCTTTAAGCAATC 2880
Qy 1081 AAGGGGGGGAGACATCTCATCTTCTGCACTCAAAAGAGAGTGGACGAGCTCGCGCA 1140
Db 2881 AAGGGGGGGAGACATCTCATCTTCTGCACTCAAAAGAGAGTGGATGAGCTCGCGCG 2940
Qy 1141 AAACCTGTGCGCTTGGGCGCTCAATGCGGCTTACCTACCGCGCTTGTGTCTGCTC 1200
Db 2941 AAGCTGTGCGGCTCGGACTCATGTGCTGATATTAACCGGGGCTTGTATCTGCTC 3000
Qy 1201 ATCCCGACCAAGTGTGACCTTGTCTGTGTGGCACTGAGCCCTCATGACCGGCTTTTAC 1260
Db 3001 ATACCAACTGAGCGGAGACGTCAATGTCTGAGCAAGGAGCTCTAATGACGGGCTTTTAC 3060
Qy 1261 GCGCATCTTGATTCGGTGTATGACTGCAACAGTGTGTACCCGACAGTCCACTTACG 1320
Db 3061 GCGCATCTTGATTCAGTGTATGCACTGCAATATGTGTACCCGACAGTCCACTTACG 3120
Qy 1321 CTGACCCCTTACCTTACCATGAGACATACAGCTTCCGAGATGTGTCTCCGCTACT 1380
Db 3121 CTGACCCGACCTTACCATGAGACAGACCGGTGCCAAGACGGGCTGTCAAGCTGC 3180
Qy 1381 CAACCTCGGGGTGAGACTGGCAGAGAGGAGCCAGAGATCTAAGATTTGTGGACCGGG 1440
Db 3181 CAGCGCGGAGGAGACTGGTGTAGGGGAGAGATGGGATTTTAAAGTTGTGACTCAAGA 3240
Qy 1441 GAGCGTCTCTTGGCACTGTTTGACTGTGTCTCTGTGAGTGTATGACCGGGTGT 1500
Db 3241 GAAACGGCTCTGGGCACTGTTTGAATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3300
Qy 1501 GCTTGTATGAGCTTACCGCCGCGGAGACCAAGTTAGGCTACGAGCATATGAACCC 1560
Db 3301 GCTTGTATGAGCTTACCGCCGCGGAGACCTCAAGTTAGGCTTACCTTAAACACA 3360
Qy 1561 CCGGACCTTCCGCTGTGCGCAAGACCTTGAATTTTGGAGGGGCTTTTACGGGTCT 1620
Db 3361 CAGAGGTGCGCTGTGCGCAAGACCTTGAAGTTTGTGGAGAGGCTTTTACAGGCTTC 3420
Qy 1621 ACCCATATGAGCGCCACTTCTTATCCAGACAAAGAGAGTGGGAAAACTTCCCTAT 1680
Db 3421 ACCCATATGAGCGCCACTTCTTGTCCAGACTAAGAGAGAGAGACAACTTCCCTATC 3480
Qy 1681 CTGTGAGCTTACCAAGCAACCGTGTGCGTGAAGCTCAAGCCCTTCCCGCTGTGGAG 1740
Db 3481 CTGTGAGCTTACCAAGCTACGGTGTGCGCAAGGCTCAAGGCTTCACTCATGTGGAG 3540
Qy 1741 CAGATGTGAAGTGTGTATTCGCTCAAGCCCACTTCCATGAGGCGCAACCTCTGTCT 1800
Db 3541 CAAATGTGAAGTGTCTCATACGGCTTAAAGCTTACGCTCACGGGCAACGCGCTGTG 3600
Qy 1801 TATTAAGCTGGGCGCTGTCCAGATGAAGTCAACCTTACCGCAACAGTCAAGATATATC 1860
Db 3601 TATTAAGCTGGGCGCTTCAAAACAGAGTTTACTACACACACCCCAATACAAATATATC 3660
Qy 1861 ATGAACATGTATGTGGCTGACCTGAGAGTGTCTACAGAGTACCTGGGTGTCTGTGGCG 1920
Db 3661 ATGGCATGTATGTGGCTGACCTGAGAGTGTCTACAGAGCACTGGGTGTCTGTGGCGGA 3720

Qy 1921 GTTCGTGCTGCTTTGGCGCGATATGCTTATCCACAGGCTGTGTATAGTAGTAG 1980
Db 3721 GTTCGTGAGCTCTGCGCGGCTATGCTTGTACACAGGCAAGCTGTATGTGGCAG 3780
Qy 1981 ATGTCTTGTCCGGAAGACCGGCAATCATATCCGACAGGGAAGTCTTACCGGAGTTT 2040
Db 3781 ATCATCTTGTCCGGAAGACCGGCAATCATATCCGACAGGGAAGTCTTACCGGAGTTT 3840
Qy 2041 GATGAATGGAAGAGTGC 2058
Db 3841 GATGAGATGAAGAGTGC 3858

RESULT 14
US-10-509-921-13
; Sequence 13, Application US/10509921
; Publication No. US20050250093A1
; GENERAL INFORMATION:
; APPLICANT: SmithKline Beecham Corporation
; TITLE OF INVENTION: Hepatitis C Virus Sub-Genomic Replicons
; FILE REFERENCE: P51335
; CURRENT APPLICATION NUMBER: US/10/509,921
; PRIOR FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: 60/369,685
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 7989
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The polynucleotide sequence encodes sequences from
; US-10-509-921-13

Query Match 67.0%; Score 1381.2; DB 7; Length 7989;
Best Local Similarity 79.4%; Pred. No. 0;
Matches 1635; Conservative 0; Mismatches 423; Indels 0; Gaps 0;

Qy 1 ATGGCGCTTATCACGGCTTATGCCCCAGACGACAAAGGGGCTTTTGGATGATATCAC 60
Db 1801 ATGGCGCTTATCACGGCTTATGCCCCAGACGACGAGGCTTATGCTGATCATCACT 1860
Qy 61 AGCTTGACCGGCGCGGAGCAAAAACAGGTGAGGTGAGGTTCATATGTCATCTGCT 120
Db 1861 AGCTTGACCGGCGCGGAGCAAAAACAGGTGAGGTGAGGTTCATATGTCATCTGCT 1920
Qy 121 GCCGACCTTCTTGGCAACCTGATTAACGGGGGTGTGTGGACTGTCTAACATGAGAG 180
Db 1921 ACACATCTTCTTCTGCGACCTGCTGATGATGCTGTGTGTGATCTGTCTATATG 1980
Qy 181 GGAAACAGACCATTTGCTACCTTAAAGGCTCTGTATTCAGATGTACCAATGTGAC 240
Db 1981 GGCTCAAAAGACCTTGGCGGCGCCAAAGGGGCCAATCAACCAATGTGAGC 2040
Qy 241 CAAAGCTCTGTAGGTGTGGCCGCTCCCAAGGTGCGGCTATTAACATGACATTC 300
Db 2041 CAGGACCTGTGTGCTGCGCAAGCGGCGGCGGCGGCTTCTTGAACACATGACCTGC 2100
Qy 301 GGCTCTGGAACCTTATCTGGTTCAGAGGCAAGCGCGATGTCAATCTGTGGCGGAG 360
Db 2101 GGCACTTGGACCTTATCTTGTGTACAGAGGCAATGCGGATGTATTCGGGTGCG 2160
Qy 361 GGTGATGAGGAGGAGCTGTCTTGTGCGCGGCTTATCTTACTTGAAGGCTCTGC 420
Db 2161 GGCGACAGAGGAGGAGCTACTCTTCCCGAGGCGGCTCTTACTTGAAGGCTCTGC 2220
Qy 421 GGAAGCCCTCTGTGTGTGCGCGGAGAGACATGCGGTGAGCATTTCAAGACCGCGGTAT 480
Db 2221 GGCGGTCACTGTCTGTGCGGCGGAGAGCTGTGTGAGCATCTTTCGGGCTGCGGTGC 2280

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QY 481 ACCGCTGAGTGGCTAAGACGCGTGAATTCATCCCGTAGAGAGCTTAGACAAACATG 540
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Db 2281 ACCGAGGGGTTTGCAGAGCGGTGACCTTTGTAACCGCTGAGTCTATGAGAAACCTATG 2340
QY 541 AGGTCCCGGTTTCTCAGACAACTCTCCCAACGAGTGGCCCAAGCTAACCAATG 600
   |||||
Db 2341 CGGTCCCGGTTTCTCAGAGCAACTGTCCTCCGCGGTATCCGACAGCATTTCCAGGTG 2400
QY 601 GCCCACTGATGCTCCCAACGCGGAGGTAGACACCAAGTCCCGCGCATATCCCA 660
   |||||
Db 2401 GCCCATCTACACGCCCCCTACTGTTAGCGGACAGACACTTAAGTCCCGCTGCTATCA 2460
QY 661 GCTCAGGCTCAAGAGTGTGCTCAACCCCTCGTTGTCGACAAATGAGGCTTTGAT 720
   |||||
Db 2461 GCCCAAGGTTATAGGTGCTTGTCTGAAACCGCTCCGTGCGCCACCTTAGGTTTCGGG 2520
QY 721 GCTTACATGTCGAGGCGCAATGAGATTGATCTTAAATCAGAGCTGGGGTGAAGCAATT 780
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Db 2521 GCGTATATGTCTAAGGACATGTTATGACCTTAATCAGAAACCGGGGTAAAGACATC 2580
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Db 2581 ACCAAGGGTGGCCCCATACGATCTCACCTAATGGAAGTTCTTGGCGAGCTGTGTC 2640
QY 841 TCAGGGGGTGTATGACATTAATTTGTGACGAGTGCACCTCCAGGATGCAATCC 900
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Db 2641 TCTGGGGGCGCTTATGACATCTAATTAATGATGATGCTCACTCAATGATCTGCAACT 2700
QY 901 ATCTTGGGCAATTTGGCACTGTCTTTCAGCAAGCAGACCGCGGGGCGAGACTGTG 960
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QY 1081 AAGGGGGGAGACATCTCATCTTCTGCACTCAAGAAAGAAAGTGGAGAGCTCGCCGA 1140
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Db 2881 AAGGGGGGAGACATCTCATCTTCTGCACTCAAGAAAGAAAGTGGAGAGCTCGCCGA 1140
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QY 1501 GCTTGTATGAGCTTAAGCGCCCGGAGACAGATTTAGGCTGAGACATATGAACACC 1560
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QY 1861 ATGACATGATGTGGCTGACCTGGAGGTCGTCAAGATTCCTGGGCTGCTGGCGGAC 1920
   |||||
Db 3661 ATGACATGATGTGGCTGACCTGGAGGTCGTCAAGATTCCTGGGCTGCTGGCGGAC 1920
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QY 1981 ATGTCTTGTCCGGAACCGGCAATCATPACCCAGAGGAAGTCTCTACCGGAGTTC 2040
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RESULT 15
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; Sequence 14, Application US/10509921
; Publication No. US20050250093A1
; GENERAL INFORMATION:
; APPLICANT: SmithKline Beecham Corporation
; TITLE OF INVENTION: Hepatitis C Virus Sub-Genomic Replicons
; FILE REFERENCE: P51335
; CURRENT APPLICATION NUMBER: US/10/509,921
; PRIOR FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: 60/369,685
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 7989
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The polynucleotide sequence encodes sequences from
; US-10-509-921-14

Query Match 67.0%; Score 1381.2; DB 7; Length 7989;
Best Local Similarity 79.4%; Pred. No. 0;
Matches 1635; Conservative 0; Mismatches 423; Indels 0; Gaps 0;

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Job time : 403 secs

Pending Nucleic Acid and Pending Amino Acid database searches generate two sets of results each. The Pending databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches. Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions .rapm and .rapn. Searches run against the Amino Acid Pending database produce two sets of results, with the extensions .rapm and .rapn.

Because they contain data that is confidential, the results of Pending database searches should not be left in the case.

THE
GODDARD
BOOK CO.
NEW YORK

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 7, 2006, 20:23:15 : Search time 11527 Seconds
(without alignments)
9886.002 Million cell updates/sec

Title: US-10-817-591-16

Perfect score: 2061

Sequence: 1 atggcgcctacacgacctc.....atgaatggaagagtgctga 2061

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 79147668 seqs, 27645789525 residues 158295336

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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| Result No. | Score | Query Match | Length | ID | Description |
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| 2 | 2061 | 100.0 | 2061 | US-10-817-591-16 | Sequence 16, Appli |
| 3 | 2061 | 100.0 | 2061 | US-11-043-808-1 | Sequence 1, Appli |
| 4 | 2061 | 100.0 | 2061 | US-11-249-893-1 | Sequence 1, Appli |
| 5 | 2061 | 100.0 | 2061 | US-60-685-014-1 | Sequence 1, Appli |
| 6 | 2061 | 100.0 | 2061 | US-60-685-015-163 | Sequence 163, App |
| 7 | 1787 | 86.7 | 6299 | US-09-721-479B-6 | Sequence 6, Appli |
| 8 | 1787 | 86.7 | 6299 | US-11-195-009-6 | Sequence 6, Appli |
| 9 | 1786 | 86.7 | 7310 | US-08-403-590B-74 | Sequence 74, Appli |
| 10 | 1786 | 86.7 | 7310 | US-08-444-112-74 | Sequence 74, Appli |
| 11 | 1786 | 86.7 | 9229 | US-08-436-966-1 | Sequence 1, Appli |
| 12 | 1786 | 86.7 | 9379 | US-07-722-489-497 | Sequence 497, App |
| 13 | 1786 | 86.7 | 9401 | PCT-US03-19834-1 | Sequence 1, Appli |
| 14 | 1786 | 86.7 | 9401 | US-10-445-724-1 | Sequence 1, Appli |
| 15 | 1784.4 | 86.6 | 6785 | US-08-403-590B-65 | Sequence 65, Appli |
| 16 | 1784.4 | 86.6 | 6785 | US-08-444-112-65 | Sequence 65, Appli |
| 17 | 1784.4 | 86.6 | 8316 | US-08-403-590B-88 | Sequence 88, Appli |
| 18 | 1784.4 | 86.6 | 8316 | US-08-444-112-88 | Sequence 88, Appli |
| 19 | 1784.4 | 86.6 | 8987 | US-08-403-590B-137 | Sequence 137, App |
| 20 | 1784.4 | 86.6 | 8987 | US-08-444-112-137 | Sequence 137, App |
| 21 | 1784.4 | 86.6 | 9185 | US-08-403-590B-122 | Sequence 122, App |
| 22 | 1784.4 | 86.6 | 9185 | US-08-403-590B-123 | Sequence 123, App |
| 23 | 1784.4 | 86.6 | 9185 | US-08-444-112-122 | Sequence 122, App |

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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27 1781.2 86.4 2058 1 PCT-US03-28071-1 Sequence 1, Appl1
28 1781.2 86.4 2058 54 US-10-643-853-2 Sequence 2, Appl1
29 1781.2 86.4 2058 54 US-10-658-782-1 Sequence 1, Appl1
30 1781.2 86.4 5360 14 US-08-403-590B-53 Sequence 53, Appl1
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32 1781 86.4 2061 3 PCT-US05-10325-1 Sequence 1, Appl1
33 1781 86.4 2061 72 US-11-213-326-1 Sequence 1, Appl1
34 1779.6 86.3 2058 3 PCT-US05-10324-5 Sequence 5, Appl1
35 1779.6 86.3 2058 62 US-10-899-715-1 Sequence 1, Appl1
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38 1774.8 86.1 12980 38 US-09-963-433-5 Sequence 5, Appl1
39 1774.8 86.1 12980 39 US-09-995-937-5 Sequence 5, Appl1
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43 1773.2 86.0 9646 39 US-09-995-937-1 Sequence 1, Appl1
44 1766.2 85.7 11240 3 PCT-US04-40120-13 Sequence 13, Appl1
45 1765.2 85.6 9599 1 PCT-US03-21002-13 Sequence 13, Appl1

ALIGNMENTS

RESULT 1
US-10-307-047-1
Sequence 1, Application US/10307047
GENERAL INFORMATION:
APPLICANT: Matti Sallberg
TITLE OF INVENTION: A HEPATITIS C VIRUS NON-STRUCTURAL
TITLE OF INVENTION: NS3/4A FUSION GENE
FILE REFERENCE: TRIEP-028CPI
CURRENT APPLICATION NUMBER: US/10/307,047
CURRENT FILING DATE: 2002-11-26
PRIOR APPLICATION NUMBER: 60/225,767
PRIOR FILING DATE: 2000-08-17
PRIOR APPLICATION NUMBER: 60/229,175
PRIOR FILING DATE: 2000-08-29
PRIOR APPLICATION NUMBER: 09/705,547
PRIOR FILING DATE: 2000-11-03
PRIOR APPLICATION NUMBER: 09/930591
PRIOR FILING DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FaSTSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 2061
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Hepatitis C virus NS3/4A coding region
US-10-307-047-1

Query Match 100.0%; Score 2061; DB 48; Length 2061;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2061; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 181 GGACAGAGACATTTGCTGCTACCTAAGGCTCTGTTATCCAGATGTACCAATGTGAC 240

DB 181 GGACAGAGACATTTGCTGCTACCTAAGGCTCTGTTATCCAGATGTACCAATGTGAC 240
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QY 421 GGAGGCGCTCTGCTGTGCGCGAGAGATGCGGATGCAATTAAGAGCGCGGATGAC 480
DB 421 GGAGGCGCTCTGCTGTGCGCGAGAGATGCGGATGCAATTAAGAGCGCGGATGAC 480
QY 481 ACCGTGAGTGTGCTTAAGGCGGTGACTTTCATCCCGTATGAGAGCTTGAAGCAACATG 540
DB 481 ACCGTGAGTGTGCTTAAGGCGGTGACTTTCATCCCGTATGAGAGCTTGAAGCAACATG 540
QY 541 AGCTCCCGGTGTTCTCAAGACATCTCTCCCAACAGAGCTGCCAGAGCTACCAAGTG 600
DB 541 AGCTCCCGGTGTTCTCAAGACATCTCTCCCAACAGAGCTGCCAGAGCTACCAAGTG 600
QY 601 GCCGACCTGATGCTCCAGCGGAGCGGTAAGAGCAACAGGTCGCGGCGATACGCA 660
DB 601 GCCGACCTGATGCTCCAGCGGAGCGGTAAGAGCAACAGGTCGCGGCGATACGCA 660
QY 661 GCTCAGGCTACAGAGTCTGTGCTCAACCCCTCGTGTGCAACAAATGAGCTTTGCT 720
DB 661 GCTCAGGCTACAGAGTCTGTGCTCAACCCCTCGTGTGCAACAAATGAGCTTTGCT 720
QY 721 GCTTACATGTGCAAGGCGGCAATGATGATCTTAATCAAGAGCTGGGTGAGCAAT 780
DB 721 GCTTACATGTGCAAGGCGGCAATGATGATCTTAATCAAGAGCTGGGTGAGCAAT 780
QY 781 ACTACTGAGGCGGATACGATTCACGATTCACGAGGCAAGTCTTGGCGAGCGGAGTGT 840
DB 781 ACTACTGAGGCGGATACGATTCACGATTCACGAGGCAAGTCTTGGCGAGCGGAGTGT 840
QY 841 TCAGGAGGCTTATGACATATAATTTGTGACAGTGTGCACTCCAGGATGCAACATCC 900
DB 841 TCAGGAGGCTTATGACATATAATTTGTGACAGTGTGCACTCCAGGATGCAACATCC 900
QY 901 ATCTTGGGCTATGAGCACTGTCTTGAACCAAGGAGACCGCGGCGAGCTGACTGTG 960
DB 901 ATCTTGGGCTATGAGCACTGTCTTGAACCAAGGAGACCGCGGCGAGCTGACTGTG 960
QY 961 CTGCGCACCGCTACCCCTCCGCGGCTCGGTCACTGTGCGCCCATCTTAACATGAGAGT 1020
DB 961 CTGCGCACCGCTACCCCTCCGCGGCTCGGTCACTGTGCGCCCATCTTAACATGAGAGT 1020
QY 1021 GCTCTGTCACTACCGAGAGATCCCTTTATGCGAAGCTATTCCTCTTAAGCAAT 1080
DB 1021 GCTCTGTCACTACCGAGAGATCCCTTTATGCGAAGCTATTCCTCTTAAGCAAT 1080
QY 1081 AAGGGGGGAGACATCTCATCTTTCGCACTCAAGAAAGAAAGTGGAGAGAGCTCCCGCA 1140
DB 1081 AAGGGGGGAGACATCTCATCTTTCGCACTCAAGAAAGAAAGTGGAGAGAGCTCCCGCA 1140
QY 1141 AAACGTGTGCGGTGAGGAGTCAATGCGGTGCTTCACTCCGCGGCTTATGATGTCCGT 1200
DB 1141 AAACGTGTGCGGTGAGGAGTCAATGCGGTGCTTCACTCCGCGGCTTATGATGTCCGT 1200
QY 1201 ATCCGACCAAGTGTGAGCTGTGCTGTGCGCACTGACGCGCTATGACCGGCTTTTAC 1260
DB 1201 ATCCGACCAAGTGTGAGCTGTGCTGTGCGCACTGACGCGCTATGACCGGCTTTTAC 1260
QY 1261 GCGGACTTGTGATGCTGTATGAGCTGCAACAGTGTGTCAACCAAGCACTGACTTAC 1320
DB 1261 GCGGACTTGTGATGCTGTATGAGCTGCAACAGTGTGTCAACCAAGCACTGACTTAC 1320

QY 1321 CTGACCTACCTTACCATGAGCAATCAGCTTCCCGAGATGCTCCCGTACT 1380
 DB 1321 CTGACCTTACCTTACCATGAGCAATCAGCTTCCCGAGATGCTCCCGTACT 1380
 QY 1381 CAACGTCCGGGGTGAAGCTGGCAGAGGAAAGCCAGCATCTACAGATTGTGGCAGCGGG 1440
 DB 1381 CAACGTCCGGGGTGAAGCTGGCAGAGGAAAGCCAGCATCTACAGATTGTGGCAGCGGG 1440
 QY 1441 GAGCGTCTTCTGGCATGTTTGAATCTGCTCTCTGAGTGTCTATGACCGGGTGT 1500
 DB 1441 GAGCGTCTTCTGGCATGTTTGAATCTGCTCTCTGAGTGTCTATGACCGGGTGT 1500
 QY 1501 GCTTGATGAGCTTACCGCCGCGGAGACACAGTTAGGCTACGACATACAGAACACC 1560
 DB 1501 GCTTGATGAGCTTACCGCCGCGGAGACACAGTTAGGCTACGACATACAGAACACC 1560
 QY 1561 CCGGACTTCCCGTGTGCGCAAGCAATCTTGAATTTGGAGGGGCTTTTACGGGGTCTC 1620
 DB 1561 CCGGACTTCCCGTGTGCGCAAGCAATCTTGAATTTGGAGGGGCTTTTACGGGGTCTC 1620
 QY 1621 ACCCATATGACGCCCATCTTCTATCCAGACAAAGCAGAGTGGGAAAACTTCCCTAT 1680
 DB 1621 ACCCATATGACGCCCATCTTCTATCCAGACAAAGCAGAGTGGGAAAACTTCCCTAT 1680
 QY 1681 CTGGTAGGCTACCAAGCCACCGGTGCGCTAGAGCTCAAGCCCTCCCGGTGGGAGC 1740
 DB 1681 CTGGTAGGCTACCAAGCCACCGGTGCGCTAGAGCTCAAGCCCTCCCGGTGGGAGC 1740
 QY 1741 CAGATGGAAGTGTGATCGCTCTCAAGCCCATCTTCATGAGGCAACCTCTGCTA 1800
 DB 1741 CAGATGGAAGTGTGATCGCTCTCAAGCCCATCTTCATGAGGCAACCTCTGCTA 1800
 QY 1801 TATAGACTGGGCGCTGTCCAGATGAAGTCACTTGAAGCCAGTCAAGATATATC 1860
 DB 1801 TATAGACTGGGCGCTGTCCAGATGAAGTCACTTGAAGCCAGTCAAGATATATC 1860
 QY 1861 ATGACATGATGTCGGCTGACCTGAGAGGCTCAAGATGCTGGGTGCTCGTGGCGGC 1920
 DB 1861 ATGACATGATGTCGGCTGACCTGAGAGGCTCAAGATGCTGGGTGCTCGTGGCGGC 1920
 QY 1921 GTTCTGCTGCTTGTGGCCGCGATATGCTATCCACAGGCTGGGTGCTATGATGATG 1980
 DB 1921 GTTCTGCTGCTTGTGGCCGCGATATGCTATCCACAGGCTGGGTGCTATGATGATG 1980
 QY 1981 ATTGCTTGTCCGAAAGCCGCAATCATACCCGACAGGAAAGTCTTACCGGAGTTC 2040
 DB 1981 ATTGCTTGTCCGAAAGCCGCAATCATACCCGACAGGAAAGTCTTACCGGAGTTC 2040
 QY 2041 GATGAATGGAAGTGTCTGA 2061
 DB 2041 GATGAATGGAAGTGTCTGA 2061

RESULT 2
 US-10-817-591-16
 ; Sequence 16, Application US/10817591

; GENERAL INFORMATION:
 ; APPLICANT: Macti Salilberg
 ; APPLICANT: Catharina Hulcyren
 ; TITLE OF INVENTION: VACCINES CONTAINING RIBAVIRIN AND
 ; TITLE OF INVENTION: METHODS OF USE THEREOF
 ; FILE REFERENCE: TRIPEP 23AUS2C1
 ; CURRENT APPLICATION NUMBER: US/10/817,591
 ; PRIOR FILING DATE: 2004-04-02
 ; PRIOR FILING DATE: 2003-11-20
 ; PRIOR FILING DATE: 2003-11-20
 ; PRIOR FILING DATE: 2002-03-22
 ; PRIOR APPLICATION NUMBER: 09/929,955
 ; PRIOR FILING DATE: 2001-08-15
 ; PRIOR APPLICATION NUMBER: 09/705,547
 ; PRIOR FILING DATE: 2000-11-03

; PRIOR APPLICATION NUMBER: 60/229,175
 ; PRIOR FILING DATE: 2000-08-29
 ; PRIOR APPLICATION NUMBER: 60/225,767
 ; PRIOR FILING DATE: 2000-08-17
 ; NUMBER OF SEQ ID NOS: 49
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 16
 ; LENGTH: 2061
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Hepatitis C virus NS3/4A coding region
 US-10-817-591-16

Query Match 100.0%; Score 2061; DB 62; Length 2061;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2061; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCGCTATACCGGCTTATGCGCAGAGACAAAGGGCTTTTGGATGATTAATCAC 60
 DB 1 ATGGCGCTATACCGGCTTATGCGCAGAGACAAAGGGCTTTTGGATGATTAATCAC 60
 QY 61 AGCTTACCGGCGGAGCAAAAAACAGGTGAGGTGAGTTCAATGCTTCAACTGCT 120
 DB 61 AGCTTACCGGCGGAGCAAAAAACAGGTGAGGTGAGTTCAATGCTTCAACTGCT 120
 QY 121 GCCCAGACTTTCTTGGCAACCTGCAATTAACGGGGTGTGTGGAATGCTACATGAGGCC 180
 DB 121 GCCCAGACTTTCTTGGCAACCTGCAATTAACGGGGTGTGTGGAATGCTACATGAGGCC 180
 QY 181 GGAACAAGAACATTGCGTCACTAAGGCTCTGTTATCAGATGTACACCAATGTGAC 240
 DB 181 GGAACAAGAACATTGCGTCACTAAGGCTCTGTTATCAGATGTACACCAATGTGAC 240
 QY 241 CAAGAATTGTAAGCTGAGCTGCTCCCAAGGTGCGGCTCAATTAACCATGACTTGC 300
 DB 241 CAAGAATTGTAAGCTGAGCTGCTCCCAAGGTGCGGCTCAATTAACCATGACTTGC 300
 QY 301 GGCTCTCGGACCTTTACTGTGTACAGAGCAGCGGCAATTCCTGTGGCGGAGCG 360
 DB 301 GGCTCTCGGACCTTTACTGTGTACAGAGCAGCGGCAATTCCTGTGTGGCGGAGCG 360
 QY 361 GGTGATGAGGAGGAGCAGCTGCTTGCCTCCGCGCTATCTCTTACTTGAAGGCTCTCG 420
 DB 361 GGTGATGAGGAGGAGCAGCTGCTTGCCTCCGCGCTATCTCTTACTTGAAGGCTCTCG 420
 QY 421 GGAGGCGCTTGTGCTGCTGCTCCGAGACATGCGGTAGCATTAAGACCGCGGTATGC 480
 DB 421 GGAGGCGCTTGTGCTGCTGCTCCGAGACATGCGGTAGCATTAAGACCGCGGTATGC 480
 QY 481 ACCCGTGAAGTGGCTTAAGCGGTGATTCATCCCGTATGAGAGCTTATGAGCAACCATG 540
 DB 481 ACCCGTGAAGTGGCTTAAGCGGTGATTCATCCCGTATGAGAGCTTATGAGCAACCATG 540
 QY 541 AGGTCCCGGTGTTCTCAGACAACTCTCCACAGAGTGCCTCCAGAGTACCAAGTG 600
 DB 541 AGGTCCCGGTGTTCTCAGACAACTCTCCACAGAGTGCCTCCAGAGTACCAAGTG 600
 QY 601 GCCCATCTGATGCTCCACCGGAGCGGTAAAGACCAAGATCCCGGCGCATACGCA 660
 DB 601 GCCCATCTGATGCTCCACCGGAGCGGTAAAGACCAAGATCCCGGCGCATACGCA 660
 QY 661 GCTCAGGGCTAACAGTGTGTGTCAACCCCTCGTGTGCAACAATGGGCTTTGT 720
 DB 661 GCTCAGGGCTAACAGTGTGTGTGTCAACCCCTCGTGTGCAACAATGGGCTTTGT 720
 QY 721 GCTTACATGTCGAAGGCCATGAGATTGATCTTAACATCAGAGCTGGGGTGAAGCAAT 780
 DB 721 GCTTACATGTCGAAGGCCATGAGATTGATCTTAACATCAGAGCTGGGGTGAAGCAAT 780
 QY 781 ACTACTGAGCGCGGATCAAGTATTCATCAGGCAAGTTCTTGGCGAGCGGGGTGT 840
 DB 781 ACTACTGAGCGCGGATCAAGTATTCATCAGGCAAGTTCTTGGCGAGCGGGGTGT 840

QY 841 TCAGGGGGGCTTATGACATTAATTTTGAAGAGTGCACCTCCAGGATGCAATCC 900
DB 841 TCAGGGGGGCTTATGACATTAATTTTGAAGAGTGCACCTCCAGGATGCAATCC 900
QY 901 ATCTTGGGCAATGGGCACTGTCTTGAACAAGAGAGCCGGGGGAGACTGTG 960
DB 901 ATCTTGGGCAATGGGCACTGTCTTGAACAAGAGAGCCGGGGGAGACTGTG 960
QY 961 CTGCGCACCGCTAACCCCTCCGGCTCCGCTACCTGTGCCCCATCTAATCAGAGGTT 1020
DB 961 CTGCGCACCGCTAACCCCTCCGGCTCCGCTACCTGTGCCCCATCTAATCAGAGGTT 1020
QY 1021 GCTGTGCTACCTACCGGAGAGATCCCTTTATGGCAGGCTATTCCCTTGAAGCAATT 1080
DB 1021 GCTGTGCTACCTACCGGAGAGATCCCTTTATGGCAGGCTATTCCCTTGAAGCAATT 1080
QY 1081 AAGGGGGGAGACATCTCATCTTCTGCACTCAAGAGAGAGTGCACGAGCTCGCGCA 1140
DB 1081 AAGGGGGGAGACATCTCATCTTCTGCACTCAAGAGAGAGTGCACGAGCTCGCGCA 1140
QY 1141 AAACGTGTGCGTGGGCGTCAATGCGGTGCTTACTACCGGCGCTTATGTGCTG 1200
DB 1141 AAACGTGTGCGTGGGCGTCAATGCGGTGCTTACTACCGGCGCTTATGTGCTG 1200
QY 1201 ATCCGACCAAGTGAAGTGTGCGTGTGCGCACTGACGCGCTCATGACGCGCTTTACC 1260
DB 1201 ATCCGACCAAGTGAAGTGTGCGTGTGCGCACTGACGCGCTCATGACGCGCTTTACC 1260
QY 1261 GCGCATCTTGATTCGGTGTATAGACTGCAACAGTGTGTCAACAGTGTGCACTTAC 1320
DB 1261 GCGCATCTTGATTCGGTGTATAGACTGCAACAGTGTGTCAACAGTGTGCACTTAC 1320
QY 1321 CTGACACCTTACCTTACCAATTGAGACATCAAGCTTCCCAAGATGCTGTCTCCGTACT 1380
DB 1321 CTGACACCTTACCTTACCAATTGAGACATCAAGCTTCCCAAGATGCTGTCTCCGTACT 1380
QY 1381 CAACGTGCGGGTGAAGACTGAGAGAGAGAGCCAGGATCTAAGATTTTGGACCGGGG 1440
DB 1381 CAACGTGCGGGTGAAGACTGAGAGAGAGAGCCAGGATCTAAGATTTTGGACCGGGG 1440
QY 1441 GAGCGCTCTTGTGCAATGTTTGAATGCTGTCTCTGCAAGTGTATGACCGGGTGT 1500
DB 1441 GAGCGCTCTTGTGCAATGTTTGAATGCTGTCTCTGCAAGTGTATGACCGGGTGT 1500
QY 1501 GCTTGTATGAGCTTAAGCCCGCGAGACCAAGTGAAGCTAAGACATTAAGAAC 1560
DB 1501 GCTTGTATGAGCTTAAGCCCGCGAGACCAAGTGAAGCTAAGACATTAAGAAC 1560
QY 1561 CCGGGGCTCCCGGTGTGCAAGACATCTTGAATTTTGGAGGGGCTTTTACGGGCTC 1620
DB 1561 CCGGGGCTCCCGGTGTGCAAGACATCTTGAATTTTGGAGGGGCTTTTACGGGCTC 1620
QY 1621 ACCCATATGAGACGCCCATCTTCTATCCAGACAAAGAGAGTGGGAAAACTTCCCTAT 1680
DB 1621 ACCCATATGAGACGCCCATCTTCTATCCAGACAAAGAGAGTGGGAAAACTTCCCTAT 1680
QY 1681 CTGCTGAGCTTACCAAGCCACGCTGTGCTAAGAGCTCAAGCCCTTCCCGTGTGGAC 1740
DB 1681 CTGCTGAGCTTACCAAGCCACGCTGTGCTAAGAGCTCAAGCCCTTCCCGTGTGGAC 1740
QY 1741 CAGATGTGAAGTGTGATTCGCTCAAGCCCAACCTCATGGGCAACACTCTGCTA 1800
DB 1741 CAGATGTGAAGTGTGATTCGCTCAAGCCCAACCTCATGGGCAACACTCTGCTA 1800
QY 1801 TATAGACTGGGCGCTGTCCAGATGAAGTCAACCTTGAAGCAACCAAGTATATC 1860
DB 1801 TATAGACTGGGCGCTGTCCAGATGAAGTCAACCTTGAAGCAACCAAGTATATC 1860
QY 1861 ATGACATGTATGTGGGCTGACCTGAGAGTGTGTCAGAGTACTGGGTGCTGTTGGCGGC 1920
DB 1861 ATGACATGTATGTGGGCTGACCTGAGAGTGTGTCAGAGTACTGGGTGCTGTTGGCGGC 1920

QY 1921 GTTCTGCTGCTTTGGCCCGGATATCTATCCAGGCTGCGTGTATAGTAGG 1980
DB 1921 GTTCTGCTGCTTTGGCCCGGATATCTATCCAGGCTGCGTGTATAGTAGG 1980
QY 1981 ATGTCTTGTCCGGAAGCCCGCAATCATACCAGAGGAGTCTTACCGGAGTTTC 2040
DB 1981 ATGTCTTGTCCGGAAGCCCGCAATCATACCAGAGGAGTCTTACCGGAGTTTC 2040
QY 2041 GATGAATGGAAGAGTGTGA 2061
DB 2041 GATGAATGGAAGAGTGTGA 2061

RESULT 3

US-11-043-808-1
; Sequence 1, Application US/11043808
; GENERAL INFORMATION:
; APPLICANT: Macti Saliberg
; TITLE OF INVENTION: A HEPATITIS C VIRUS CODON OPTIMIZED
; FILE REFERENCE: TRIPEP.028P1C1
; CURRENT APPLICATION NUMBER: US/11/043,808
; PRIOR FILING DATE: 2005-01-25
; PRIOR APPLICATION NUMBER: 10/307,047
; PRIOR FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: 09/930,591
; PRIOR FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: 09/929,955
; PRIOR FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: 09/930,591
; PRIOR FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: 60/225,767
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/229,175
; PRIOR FILING DATE: 2000-08-29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2061
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hepatitis C virus NS3/4A coding region
US-11-043-808-1

Query Match 100.0%; Score 2061; DB 66; Length 2061;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2061; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGGCGCTATCAGCGGCTATGCGCAGGAGCAAGAGGCGCTTTGGAGATGATTAATCACC 60
DB 1 ATGGGCGCTATCAGCGGCTATGCGCAGGAGCAAGAGGCGCTTTGGAGATGATTAATCACC 60
QY 61 AGCTTGACCGGCGGGAGCAAAAAACAGGTGAAGGTGAGTTCAGATGCTGTCAACTGCT 120
DB 61 AGCTTGACCGGCGGGAGCAAAAAACAGGTGAAGGTGAGTTCAGATGCTGTCAACTGCT 120
QY 121 GCCGAGCTTTTGTGGCACTGTGCAATTAACGGGGTGTGTGGAATCTGTCAACATGAGGC 180
DB 121 GCCGAGCTTTTGTGGCACTGTGCAATTAACGGGGTGTGTGGAATCTGTCAACATGAGGC 180
QY 181 GGAACAGAGACCATTTGCGTCACTAAGGCTCTGTTATCCAGATGTAACCAATGTGAGC 240
DB 181 GGAACAGAGACCATTTGCGTCACTAAGGCTCTGTTATCCAGATGTAACCAATGTGAGC 240
QY 241 CAAGAAGCTGTAGAGTGGCGCGCTCCCAAGGTGCGCGCTCATTAACCAATGCACTTGC 300
DB 241 CAAGAAGCTGTAGAGTGGCGCGCTCCCAAGGTGCGCGCTCATTAACCAATGCACTTGC 300
QY 301 GGTCTCTGGAGACTTTACTGTGTACAGAGGCAAGCGGATGTATTCCTGTGGCCGACGG 360
DB 301 GGTCTCTGGAGACTTTACTGTGTGTACAGAGGCAAGCGGATGTATTCCTGTGGCCGACGG 360

361 GATGATGAGAGGAGAGCTCTTTGCGCCCGGCTATCTTACTTGAAGAGCTCTCG 420
Db GGTATGAGAGGAGAGCTCTTTGCGCCCGGCTATCTTACTTGAAGAGCTCTCG 420
Qy 421 GAGAGGCTCTGCTGTGCGCCGAGAGACATGCGGTAGGCAATTCAGAGCGCGGTATGC 480
Db GAGAGGCTCTGCTGTGCGCCGAGAGACATGCGGTAGGCAATTCAGAGCGCGGTATGC 480
Qy 481 ACCCGTGAAGTGGCTTAAGGCGGTGAGCTTCAATCCCGTGAAGAGCTTGAAGCAACCATG 540
Db ACCCGTGAAGTGGCTTAAGGCGGTGAGCTTCAATCCCGTGAAGAGCTTGAAGCAACCATG 540
Qy 541 AGGTCCCGGTGTTCTCAGACAACTCTCTCCAGCAGAGCTCCCGAGAGTACCAAGT 600
Db AGGTCCCGGTGTTCTCAGACAACTCTCTCCAGCAGAGCTCCCGAGAGTACCAAGT 600
Qy 601 GCCCATCTGATGCTCCACCGGAGCGGTAAAGAGCAAGAGTCCCGGCGCATACGA 660
Db GCCCATCTGATGCTCCACCGGAGCGGTAAAGAGCAAGAGTCCCGGCGCATACGA 660
Qy 661 GCTCAGGCTACAAAGTGTGTGCTCAACCCCTCCGTGCTGCAACATTTGGCTTTGGT 720
Db GCTCAGGCTACAAAGTGTGTGCTCAACCCCTCCGTGCTGCAACATTTGGCTTTGGT 720
Qy 721 GCTTACATGTCGAAGGCGCATGAGATTGATCTTAACATGAGATCTGGGTGAGACAAAT 780
Db GCTTACATGTCGAAGGCGCATGAGATTGATCTTAACATGAGATCTGGGTGAGACAAAT 780
Qy 781 ACTACTGGAGGCGCATGATTCACCTTACCGGCAAGTTCCTTCCGACGCGCGGT 840
Db ACTACTGGAGGCGCATGATTCACCTTACCGGCAAGTTCCTTCCGACGCGCGGT 840
Qy 841 TCAAGGCGGTGCTTATGACATTAATTTGTGACAGTGTCACTCCAGAGTGCACATTC 900
Db TCAAGGCGGTGCTTATGACATTAATTTGTGACAGTGTCACTCCAGAGTGCACATTC 900
Qy 901 ATCTTGGGCAATGGCACTGTCTTGAACAAGAGAGACGCGGGGAGAGCTGACTGTG 960
Db ATCTTGGGCAATGGCACTGTCTTGAACAAGAGAGACGCGGGGAGAGCTGACTGTG 960
Qy 961 CTCGCGACCGCTACCCCTCCGGGCTCCGCTCACTGTGCCCCATCTTAACATCGAGAGTT 1020
Db CTCGCGACCGCTACCCCTCCGGGCTCCGCTCACTGTGCCCCATCTTAACATCGAGAGTT 1020
Qy 1021 GCTCTGTCACTACCGGAGAGATCCCTTTTATGCAAGGCTATTCCTTGAAGCAAT 1080
Db GCTCTGTCACTACCGGAGAGATCCCTTTTATGCAAGGCTATTCCTTGAAGCAAT 1080
Qy 1081 AAGGGGGGAGACATCTCATCTTCTGCGCATCAAAAGAAAGATGGAGAGAGCTCGCGCA 1140
Db AAGGGGGGAGACATCTCATCTTCTGCGCATCAAAAGAAAGATGGAGAGAGCTCGCGCA 1140
Qy 1141 AAACCTGTGCGCTTGGGCTCAATGCGGTGCTTACTACCGGCGCTTGTATGCTCCGTC 1200
Db AAACCTGTGCGCTTGGGCTCAATGCGGTGCTTACTACCGGCGCTTGTATGCTCCGTC 1200
Qy 1201 ATCCGACCAAGTGTGAGCTTGTCTGTGCGCACTGACGCGCTTATGACCGGCTTTAC 1260
Db ATCCGACCAAGTGTGAGCTTGTCTGTGCGCACTGACGCGCTTATGACCGGCTTTAC 1260
Qy 1261 GCGGACTTGCATTCGGTGTATGAGTGCACAGTGTGTACCCGAGACAGTGCATTCAGC 1320
Db GCGGACTTGCATTCGGTGTATGAGTGCACAGTGTGTACCCGAGACAGTGCATTCAGC 1320
Qy 1321 CTGGAACCTTACCTTACATTAAGACAAATCAAGCTTCCCGAGAGTCTCTCCGTA 1380
Db CTGGAACCTTACCTTACATTAAGACAAATCAAGCTTCCCGAGAGTCTCTCCGTA 1380
Qy 1381 CAACGTCGGGGTATGAGCTGTGAGAGAGGCAAGGATCTTAAGATTTGTGACACCGGG 1440
Db CAACGTCGGGGTATGAGCTGTGAGAGAGGCAAGGATCTTAAGATTTGTGACACCGGG 1440
Qy 1441 GAGCGTCTTCTGAGATGTTGACTGTCTGTCTGTGAGTGTGATGACCGGGTGT 1500

1441 GAGCGTCTTCTGAGATGTTGACTGTGTCTCTGTGAGTGTATGACCGGGTGT 1500
Qy 1501 GCTTGTATGAGCTTACCGCCCGGAGACCAAGTTAAGCTTACAGCATATCAATGAACAC 1560
Db 1501 GCTTGTATGAGCTTACCGCCCGGAGACCAAGTTAAGCTTACAGCATATCAATGAACAC 1560
Qy 1561 CCGGAGCTTCCGCTGTGCAAGACCATCTTGAATTTTGGAGAGGCGTCTTACGGGTCTC 1620
Db 1561 CCGGAGCTTCCGCTGTGCAAGACCATCTTGAATTTTGGAGAGGCGTCTTACGGGTCTC 1620
Qy 1621 ACCCATAGACGCCCATCTTCTATCCAGACCAAGAGAGTGGGAAAACTTCCAT 1680
Db 1621 ACCCATAGACGCCCATCTTCTATCCAGACCAAGAGAGTGGGAAAACTTCCAT 1680
Qy 1681 CTGTAAGGCTACCAAGCCAGTGTGCGCTAGAGCTCAAGCCCTCCCGCTGTGGAC 1740
Db 1681 CTGTAAGGCTACCAAGCCAGTGTGCGCTAGAGCTCAAGCCCTCCCGCTGTGGAC 1740
Qy 1741 CAGATGTGAAGTGTGTGATCCGTCTCAAGCCCATCCCTCATGGGCAACACTCTGCTA 1800
Db 1741 CAGATGTGAAGTGTGTGATCCGTCTCAAGCCCATCCCTCATGGGCAACACTCTGCTA 1800
Qy 1801 TATAGACTGGGCTGTCCAGATGAGTCAACCTTGAAGCAACCAATCATATATC 1860
Db 1801 TATAGACTGGGCTGTCCAGATGAGTCAACCTTGAAGCAACCAATCATATATC 1860
Qy 1861 ATGACATGATGTGCGGCTGACCTGAGAGTCTGACAGATGCTTGGGTCTGTTGGCGG 1920
Db 1861 ATGACATGATGTGCGGCTGACCTGAGAGTCTGACAGATGCTTGGGTCTGTTGGCGG 1920
Qy 1921 GTTCTGCTGCTTGGCGCGGTATGCTTATCAAGGCTGTGCTGATAGTATGAGT 1980
Db 1921 GTTCTGCTGCTTGGCGCGGTATGCTTATCAAGGCTGTGCTGATAGTATGAGT 1980
Qy 1981 ATGTCTTGTCCGGAAGCGGCAATCATACCGGAGAGTCTTACCGGAGTTC 2040
Db 1981 ATGTCTTGTCCGGAAGCGGCAATCATACCGGAGAGTCTTACCGGAGTTC 2040
Qy 2041 GATGAATGGAAGAGTCTGA 2061
Db 2041 GATGAATGGAAGAGTCTGA 2061

RESULT 4
US-11-249-893-1
; Sequence 1, Application US/11249893
; GENERAL INFORMATION:
; APPLICANT: Matti Saljberg
; TITLE OF INVENTION: A HEPATITIS C VIRUS NON-STRUCTURAL
; FILE REFERENCE: TRIPEP.028C1
; CURRENT APPLICATION NUMBER: US/11/249.893
; PRIOR FILING DATE: 2005-10-13
; PRIOR APPLICATION NUMBER: 09/930.591
; PRIOR FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: 60/225.767
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/229.175
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2061
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hepatitis C virus NS3/4A coding region
US-11-249-893-1

Query Match 100.0%; Score 2061; DB 72; Length 2061;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2061; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGGCGCTATGACGGGCGCTATGCGGAGACAGAGAGAGGCGCTTTGGGANTGATATCAAC 60
Db 1 ATGGGCGCTATGACGGGCGCTATGCGGAGACAGAGAGAGGCGCTTTGGGANTGATATCAAC 60
QY 61 AGCTTGACCGGCGGAGACAAAAACAGGTGAGGTGAGGTTCAGATCGTGTCAACTGCT 120
Db 61 AGCTTGACCGGCGGAGACAAAAACAGGTGAGGTGAGGTTCAGATCGTGTCAACTGCT 120
QY 121 GCCGAGACTTTCTTGGCAACTGTCATTAACGGGGTGTGTGGACTGTCTACCATGAGACC 180
Db 121 GCCGAGACTTTCTTGGCAACTGTCATTAACGGGGTGTGTGGACTGTCTACCATGAGACC 180
QY 181 GGAAACAAGGACCATGCGTCACTAAGGGTCCGTTATCAGATGATGACCAATGAGAC 240
Db 181 GGAAACAAGGACCATGCGTCACTAAGGGTCCGTTATCAGATGATGACCAATGAGAC 240
QY 241 CAAGAAGCTGTAGGTGCGCGCTCCCAAGGTGCGCGCTCATTTAACCATGACCTTGC 300
Db 241 CAAGAAGCTGTAGGTGCGCGCTCCCAAGGTGCGCGCTCATTTAACCATGACCTTGC 300
QY 301 GGCTCTCGGACCTTTAATCTGTGACAGAGGACGCCGATGTCATTCTGTGCGCGAGCG 360
Db 301 GGCTCTCGGACCTTTAATCTGTGACAGAGGACGCCGATGTCATTCTGTGCGCGAGCG 360
QY 361 GGTTAGTGGAGGGGAGCGCTGCTTTCGCGCGCGCTATCTTTACTTGTAAAGGCTCTCG 420
Db 361 GGTTAGTGGAGGGGAGCGCTGCTTTCGCGCGCGCTATCTTTACTTGTAAAGGCTCTCG 420
QY 421 GAGAGCGCTCTGTGCGCGCGAGACATGCGGTAGGACATTAAGACCGCGGTATGC 480
Db 421 GAGAGCGCTCTGTGCGCGCGAGACATGCGGTAGGACATTAAGACCGCGGTATGC 480
QY 481 ACCCGTGAAGTGGCTTAAGCGGTGACATTCCTCCGTAGAGAGCTTAAAGCAACCATG 540
Db 481 ACCCGTGAAGTGGCTTAAGCGGTGACATTCCTCCGTAGAGAGCTTAAAGCAACCATG 540
QY 541 AGGTCCCGGGTGTCTCAGACAACCTCTCCGACGAGTGCAGGAGCTACCAAGTGC 600
Db 541 AGGTCCCGGGTGTCTCAGACAACCTCTCCGACGAGTGCAGGAGCTACCAAGTGC 600
QY 601 GCCCACTGTCATGCTCCACCGGAGCGGTAAAGAGACCAAGTCCCGGCGCATACGCA 660
Db 601 GCCCACTGTCATGCTCCACCGGAGCGGTAAAGAGACCAAGTCCCGGCGCATACGCA 660
QY 661 GCTCAGGGGCTAACAAGTGTGTGTGTCACACCTCCGTGTCGCAACAATGGGCTTTGGT 720
Db 661 GCTCAGGGGCTAACAAGTGTGTGTGTCACACCTCCGTGTCGCAACAATGGGCTTTGGT 720
QY 721 GCTTACATGTCCAAAGGCGCATGGATTTGATCTTAACATCAGGACTGGGGTGAACAATT 780
Db 721 GCTTACATGTCCAAAGGCGCATGGATTTGATCTTAACATCAGGACTGGGGTGAACAATT 780
QY 781 ACTTACTGGAGCGCGCATGATTCACCTTAACGCGCAAGTTCCTTGCAGCGCGGGTGT 840
Db 781 ACTTACTGGAGCGCGCATGATTCACCTTAACGCGCAAGTTCCTTGCAGCGCGGGTGT 840
QY 841 TGAAGGGGTGCTTAATGACATTAATTTGTGACAGTGCACCTCCACGAGTGCACATTC 900
Db 841 TGAAGGGGTGCTTAATGACATTAATTTGTGACAGTGCACCTCCACGAGTGCACATTC 900
QY 901 ATCTTGGGCAATTGGCACTGCTCTGACCAAGAGAGACCGGGGGGCGAGCTGACTGTG 960
Db 901 ATCTTGGGCAATTGGCACTGCTCTGACCAAGAGAGACCGGGGGGCGAGCTGACTGTG 960
QY 961 CTGCGCACCGCTACCGCTCCGGGCTCCGTCACTGTGCGCCATCTTAACATCGAGAGGTT 1020
Db 961 CTGCGCACCGCTACCGCTCCGGGCTCCGTCACTGTGCGCCATCTTAACATCGAGAGGTT 1020
QY 1021 GCTCTGTCCACTACCGGAGAGATCCCTTTTATGGCAAGGCTATTCCTCTGAAGCAATT 1080
Db 1021 GCTCTGTCCACTACCGGAGAGATCCCTTTTATGGCAAGGCTATTCCTCTGAAGCAATT 1080

QY 1081 AAGGGGGGAGACATCTCATCTTGTGCACTCAAGAAAGAGTGGAGAGCTCCGCGA 1140
Db 1081 AAGGGGGGAGACATCTCATCTTGTGCACTCAAGAAAGAGTGGAGAGCTCCGCGA 1140
QY 1141 AAACGTGTGCGGTGGGCGTCAATGCGGTGCTTAACACCGGCGCTTGAATGTCCGT 1200
Db 1141 AAACGTGTGCGGTGGGCGTCAATGCGGTGCTTAACACCGGCGCTTGAATGTCCGT 1200
QY 1201 ATCCGACCAATGGGAGAGTGTGTGTGCGTGGCAATGACGCGCTCATGACCGGCTTTACC 1260
Db 1201 ATCCGACCAATGGGAGAGTGTGTGTGCGTGGCAATGACGCGCTCATGACCGGCTTTACC 1260
QY 1261 GCGGACTTCGATTCGATGATGACTGCAACAGTGTGTCACCCAGACAGTTCGACTTCACG 1320
Db 1261 GCGGACTTCGATTCGATGATGACTGCAACAGTGTGTCACCCAGACAGTTCGACTTCACG 1320
QY 1321 CTGACCTTACCTTACCATTTAGACAAATCACGCTTCCCAAGATGTGTCTCCGTAAT 1380
Db 1321 CTGACCTTACCTTACCATTTAGACAAATCACGCTTCCCAAGATGTGTCTCCGTAAT 1380
QY 1381 CAAGGTGGGGGTAGGACTGGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1440
Db 1381 CAAGGTGGGGGTAGGACTGGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1440
QY 1441 GAGCGTCTTCTGCGATGTTTGAATCTGTCTGTCTCTGCGAGTGTGCTATGACCGGGTGT 1500
Db 1441 GAGCGTCTTCTGCGATGTTTGAATCTGTCTGTCTCTGCGAGTGTGCTATGACCGGGTGT 1500
QY 1501 GCTTGTATGACTTAAAGCGCGCGAGACACAGTTAGGCTTACGACATATGAAACACC 1560
Db 1501 GCTTGTATGACTTAAAGCGCGCGAGACACAGTTAGGCTTACGACATATGAAACACC 1560
QY 1561 CCGGAGCTTCCCGGTGTCAGAGACCATTTGAATTTGGAGGGGCTTTAGGGGTCTC 1620
Db 1561 CCGGAGCTTCCCGGTGTCAGAGACCATTTGAATTTGGAGGGGCTTTAGGGGTCTC 1620
QY 1621 ACCCATATAGAGCGCCACTTCTATCCAGACCAAGAGAGTGGGAAAACTTCCCTAT 1680
Db 1621 ACCCATATAGAGCGCCACTTCTATCCAGACCAAGAGAGTGGGAAAACTTCCCTAT 1680
QY 1681 CTGTAGCGGTACCAAGCCACCGTGTGCGTGAAGCTCAAGCCCTCCGCTGTGGGAC 1740
Db 1681 CTGTAGCGGTACCAAGCCACCGTGTGCGTGAAGCTCAAGCCCTCCGCTGTGGGAC 1740
QY 1741 CAGATGTGAAGTGTGATCCGTCTCAAGGCCACCTTCATGGGCAACACTCTGCTA 1800
Db 1741 CAGATGTGAAGTGTGATCCGTCTCAAGGCCACCTTCATGGGCAACACTCTGCTA 1800
QY 1801 TATAGACTGGGCGCTGTCCAGATGAGTCAACCTGACGACCCAGTCAACAGATATATC 1860
Db 1801 TATAGACTGGGCGCTGTCCAGATGAGTCAACCTGACGACCCAGTCAACAGATATATC 1860
QY 1861 ATGACATGATGTGCGCTGACCTGGAAGTCTGACGAGTACCTGGGTCTGTTGGCGGC 1920
Db 1861 ATGACATGATGTGCGCTGACCTGGAAGTCTGACGAGTACCTGGGTCTGTTGGCGGC 1920
QY 1921 GTTCTGGGCTGCTTGGCGCGGATGCTTATCAAGGCTGGGTGCTAATAGGTAGG 1980
Db 1921 GTTCTGGGCTGCTTGGCGCGGATGCTTATCAAGGCTGGGTGCTAATAGGTAGG 1980
QY 1981 ATTGTCTTGTCCGGAACCGGCAATCATACCCGAGAGAGTCTTACCGGGAGTTC 2040
Db 1981 ATTGTCTTGTCCGGAACCGGCAATCATACCCGAGAGAGTCTTACCGGGAGTTC 2040
QY 2041 GATGAATGAAAGAGTCTGA 2061
Db 2041 GATGAATGAAAGAGTCTGA 2061

RESULT 5
US-60-685-014-1
; Sequence 1, Application US/60685014
; GENERAL INFORMATION:

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; APPLICANT: Saliberg, Matt
; TITLE OF INVENTION: A HEPATITIS C VIRUS NON-STRUCTURAL
; FILE REFERENCE: NS3/4A FUSION GENE
; CURRENT APPLICATION NUMBER: US/60/685,014
; CURRENT FILING DATE: 2005-05-25
; NUMBER OF SEQ ID NOS: 220
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 1
; LENGTH: 2061
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hepatitis C virus NS3/4A coding region
; US-60-685-014-1

Query Match      100.0%; Score 2061; DB 82; Length 2061;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2061; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ATGGGCGCTATACAGGCGCTATATGCCCAGCAGACAAAGGGGCTTTGGAGATGATATACAC 60
DB      1 ATGGGCGCTATACAGGCGCTATATGCCCAGCAGACAAAGGGGCTTTGGAGATGATATACAC 60
QY      61 AGCTTGACCGGCGCGGACAAACAAACAGGTGAGGGTGAAGTTCAATCGTGTCAACTGCT 120
DB      61 AGCTTGACCGGCGCGGACAAACAAACAGGTGAGGGTGAAGTTCAATCGTGTCAACTGCT 120
QY      121 GCCCAGACTTTCTTGGAACAACCTGCAATTAACGGGGTGTGTGGACTGTCTACAGTGAAGCC 180
DB      121 GCCCAGACTTTCTTGGAACAACCTGCAATTAACGGGGTGTGTGGACTGTCTACAGTGAAGCC 180
QY      181 GGAACAGAGACATTTGCGTCACTTAAGGGTCTGTATATCAATATGACCAATGTGAC 240
DB      181 GGAACAGAGACATTTGCGTCACTTAAGGGTCTGTATATCAATATGACCAATGTGAC 240
QY      241 CAAAGCCTGTAGGCTGGCGCGCTCCCAAGGAGCGCGCTCATTAACACATGACACTTGC 300
DB      241 CAAAGCCTGTAGGCTGGCGCGCTCCCAAGGAGCGCGCTCATTAACACATGACACTTGC 300
QY      301 GGGCTCTGGGACCTTTACCTGTGTCAAGAGGACGCGCGATGTCTTCTGTGCGCGACGG 360
DB      301 GGGCTCTGGGACCTTTACCTGTGTCAAGAGGACGCGCGATGTCTTCTGTGCGCGACGG 360
QY      361 GGTGATGCGAGGGGAGAGCTGCTTTGCGCGCGCTATCTTACTTTGAAAGGCTCTCG 420
DB      361 GGTGATGCGAGGGGAGAGCTGCTTTGCGCGCGCTATCTTACTTTGAAAGGCTCTCG 420
QY      421 GGAGGCGCTGTGCTGTGCGCGGACAGACATGCGGTAGGCAATTCAGAGCGCGGTATGC 480
DB      421 GGAGGCGCTGTGCTGTGCGCGGACAGACATGCGGTAGGCAATTCAGAGCGCGGTATGC 480
QY      481 ACCCGTGAAGTGGCTTAAGGCGGTGACTTCATCCCGGTAGAGAGCTTAAGACAAACATG 540
DB      481 ACCCGTGAAGTGGCTTAAGGCGGTGACTTCATCCCGGTAGAGAGCTTAAGACAAACATG 540
QY      541 AGGTCCCGGTGTCTCAGACAACTCTCCCAACAGCAGTCCCGCAGAGCTACCAAGTG 600
DB      541 AGGTCCCGGTGTCTCAGACAACTCTCCCAACAGCAGTCCCGCAGAGCTACCAAGTG 600
QY      601 GCCCAGCTGCATGCTCCCAACGGGAGCGGTAAAGAGACCAAGGTCCCGCGCATATGCGA 660
DB      601 GCCCAGCTGCATGCTCCCAACGGGAGCGGTAAAGAGACCAAGGTCCCGCGCATATGCGA 660
QY      661 GCTCAAGGGGTACAAGGTGTGTGTCAACCCCTCGTTGTGCAACAATGGGCTTTTGT 720
DB      661 GCTCAAGGGGTACAAGGTGTGTGTCAACCCCTCGTTGTGCAACAATGGGCTTTTGT 720
QY      721 GCTTACATGTCCAAGGGCCATGGGATTTGATCTTAACATGAGATGCGGGGTGAGACAAT 780
DB      721 GCTTACATGTCCAAGGGCCATGGGATTTGATCTTAACATGAGATGCGGGGTGAGACAAT 780
QY      781 ACTACTGGAGCGCATTCAGATTCACGCTACCGGCAATTCCTTGGCGAGCGGGGTGT 840
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DB      781 ACTACTGGAGCGCATTCAGATTCACGCTACCGGCAATTCCTTGGCGAGCGGGGTGT 840
QY      841 TCAGGGGGTCTTATGACATTAATTTGTGACAGGTGCATCTCAACGATGCAACATCC 900
DB      841 TCAGGGGGTCTTATGACATTAATTTGTGACAGGTGCATCTCAACGATGCAACATCC 900
QY      901 ATCTTGGGCAATTGGACATGCTCTTACCAAGAGAGACCGGGGGGCGAGCTGACCTGTG 960
DB      901 ATCTTGGGCAATTGGACATGCTCTTACCAAGAGAGACCGGGGGGCGAGCTGACCTGTG 960
QY      961 CTGCGACCGCTACCCCTCCGGGCTCCGTCACTGTGCCCCATCTTAATCAGAGAGGT 1020
DB      961 CTGCGACCGCTACCCCTCCGGGCTCCGTCACTGTGCCCCATCTTAATCAGAGAGGT 1020
QY      1021 GCTCTGTCCACTACCGGAGAGATCCCTTTTATGCAAGGCTATTCCTTTAAGCAAT 1080
DB      1021 GCTCTGTCCACTACCGGAGAGATCCCTTTTATGCAAGGCTATTCCTTTAAGCAAT 1080
QY      1081 AAGGGGGGAGACATCTCATCTTCCGCACTCAAGAAAGAGTGGACGAGCTCGCGCA 1140
DB      1081 AAGGGGGGAGACATCTCATCTTCCGCACTCAAGAAAGAGTGGACGAGCTCGCGCA 1140
QY      1141 AAATGCTGCGCGTGTGGCGTCAATGCCGTGCTTACTACCGCGGCTTGATGTCCGT 1200
DB      1141 AAATGCTGCGCGTGTGGCGTCAATGCCGTGCTTACTACCGCGGCTTGATGTCCGT 1200
QY      1201 ATCCGACCAAGTGTGACGTTGTGCTGTGCACTGACGCGCTCAATGACCGGCTTTAC 1260
DB      1201 ATCCGACCAAGTGTGACGTTGTGCTGTGCACTGACGCGCTCAATGACCGGCTTTAC 1260
QY      1261 GCGGACTTCGATTCGGGTATATACGCAACAGTGTGTCAACGACAGTGTGACTTCAAC 1320
DB      1261 GCGGACTTCGATTCGGGTATATACGCAACAGTGTGTCAACGACAGTGTGACTTCAAC 1320
QY      1321 CTGGAACCTTACCTTACCAATTGAGACAAATCAAGCTTCCCAAGATGCTGTCCGTA 1380
DB      1321 CTGGAACCTTACCTTACCAATTGAGACAAATCAAGCTTCCCAAGATGCTGTCCGTA 1380
QY      1381 CAACGTGCGGGTGAAGACTGCGCAGAGAGAAACGAGCACTTAAGATTTGTGACACGGGG 1440
DB      1381 CAACGTGCGGGTGAAGACTGCGCAGAGAGAAACGAGCACTTAAGATTTGTGACACGGGG 1440
QY      1441 GAGCGTCTTCCGAGATGTTTGAATGTCGTGTGCTGTGAGTGTGATGACGCGGTGT 1500
DB      1441 GAGCGTCTTCCGAGATGTTTGAATGTCGTGTGCTGTGAGTGTGATGACGCGGTGT 1500
QY      1501 GCTGTATGAGCTTAACGCGCGCGAGACCAAGTTAGGCTACGAGCATATGAAACACC 1560
DB      1501 GCTGTATGAGCTTAACGCGCGCGAGACCAAGTTAGGCTACGAGCATATGAAACACC 1560
QY      1561 CCGGAGCTTCCGCTGTGCAAGACCATTTGAATTTGGAGGGGCTTTTACGGGCTTC 1620
DB      1561 CCGGAGCTTCCGCTGTGCAAGACCATTTGAATTTGGAGGGGCTTTTACGGGCTTC 1620
QY      1621 ACCCATATGAGGCCCATTTCTATCCAGACAAAGCAGAGTGGGGAACCTTCCCTAT 1680
DB      1621 ACCCATATGAGGCCCATTTCTATCCAGACAAAGCAGAGTGGGGAACCTTCCCTAT 1680
QY      1681 CTGTAGGCTACCAAGCCACGCTGTGCGCTAGAGCTCAAGCCCTCCCGCTGTGGAG 1740
DB      1681 CTGTAGGCTACCAAGCCACGCTGTGCGCTAGAGCTCAAGCCCTCCCGCTGTGGAG 1740
QY      1741 CAGATGTGAAGTGTGATTCGCTCAAGGCCCACTTCAAGGGCCAAACACTCTGTCTA 1800
DB      1741 CAGATGTGAAGTGTGATTCGCTCAAGGCCCACTTCAAGGGCCAAACACTCTGTCTA 1800
QY      1801 TATAGACTGGGGCTGTCCAGATATGAGTCAACCTTGAAGCAGCAGCTCAAGATATATC 1860
DB      1801 TATAGACTGGGGCTGTCCAGATATGAGTCAACCTTGAAGCAGCAGCTCAAGATATATC 1860
QY      1861 ATGACATGATGTCCGCTGACCTGAGAGTGTCAAGATACCTGTGAGTGTGCTTGGCGGC 1920
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Db 1861 ATGACATGATGTCGGCTGACCTGAGAGTGTCAACAGTACTGGGTGCTGTGGCGGC 1920
Qy 1921 GTTTCGGCTGCTTGGCGCGGATGATGCTTATCCACAGGCTGTGCTGCTATAGTAG 1980
Db 1921 GTTTCGGCTGCTTGGCGCGGATGATGCTTATCCACAGGCTGTGCTGCTATAGTAG 1980
Qy 1981 ATTGCTTGTCCGGAAGCGGCAATCATACCAGACAGGAAGTCTCTACCGGAGTTC 2040
Db 1981 ATTGCTTGTCCGGAAGCGGCAATCATACCAGACAGGAAGTCTCTACCGGAGTTC 2040
Qy 2041 GATGAATGAAAGTGTCTGA 2061
Db 2041 GATGAATGAAAGTGTCTGA 2061

RESULT 6
US-60-685-035-163
Sequence 163, Application US/60685035
GENERAL INFORMATION:
APPLICANT: Jordan, Frederick
APPLICANT: Sallberg, Matti
TITLE OF INVENTION: TRANSDERMAL FORMULATIONS CONTAINING
FILE REFERENCE: HEPATITIS C VIRUS IMMUNOGENS
CURRENT APPLICATION NUMBER: US/60/685,035
NUMBER OF SEQ ID NOS: 201
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 163
LENGTH: 2061
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Hepatitis C Virus NS3/4A coding region
US-60-685-035-163

Query Match 100.0%; Score 2061; DB 82; Length 2061;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2061; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGCGCTTATCAACGGCTATGCTCCACAGACAAAGGGGCTTTTGGGATGATTAATCACC 60
Db 1 ATGGCGCTTATCAACGGCTATGCTCCACAGACAAAGGGGCTTTTGGGATGATTAATCACC 60
Qy 61 ACCTTGACCGCGCGGAGCAAAAACAGGTGAGAGGTTCAGATCGTGTCAACTGCT 120
Db 61 ACCTTGACCGCGCGGAGCAAAAACAGGTGAGAGGTTCAGATCGTGTCAACTGCT 120
Qy 121 GCCCAGACTTCTTGGCAACCTGATTAACGGGAGTGTGATGACATGCTACCATGAGACC 180
Db 121 GCCCAGACTTCTTGGCAACCTGATTAACGGGAGTGTGATGACATGCTACCATGAGACC 180
Qy 181 GGAACAGAGACCATGCTGACCTTAAGGCTCTGTTATCAAGATGTACCAATGTGAC 240
Db 181 GGAACAGAGACCATGCTGACCTTAAGGCTCTGTTATCAAGATGTACCAATGTGAC 240
Qy 241 CAAAGACTGTAGGCTGGCGCGCTCCCAAGAGTGGCGCGCTCAATTAACCATGACCTTGC 300
Db 241 CAAAGACTGTAGGCTGGCGCGCTCCCAAGAGTGGCGCGCTCAATTAACCATGACCTTGC 300
Qy 301 GGCCTCTCGGACCTTTACCTGTGTCAAGAGGCAAGCGGATGTCACTTCTGTGCGCGAG 360
Db 301 GGCCTCTCGGACCTTTACCTGTGTCAAGAGGCAAGCGGATGTCACTTCTGTGCGCGAG 360
Qy 361 GGTGATGAGGAGGAGCGCTGCTTTGCGCGCGCTATCTTAACTTGAAGGCTCTGCG 420
Db 361 GGTGATGAGGAGGAGCGCTGCTTTGCGCGCGCTATCTTAACTTGAAGGCTCTGCG 420
Qy 421 GGAAGCGCTCTGCTGTGCCCCCAGAGACATGCGGTAGAGATTAACAGACCGCGGTATGC 480
Db 421 GGAAGCGCTCTGCTGTGCCCCCAGAGACATGCGGTAGAGATTAACAGACCGCGGTATGC 480
Qy 481 ACCCGTAGTGGCTAAAGCGGTGACTTCAATCCCGGTAGAGACTTAAGACCAACCATG 540

Db 481 ACCCGTAGTGGCTAAAGCGGTGACTTCAATCCCGGTAGAGACTTAAGACCAACCATG 540
Qy 541 AGGTCCCGGAGTGTCTCAGACAACTCTCCCAACAGAGTGTCCCAAGGCTACCAAGTG 600
Db 541 AGGTCCCGGAGTGTCTCAGACAACTCTCCCAACAGAGTGTCCCAAGGCTACCAAGTG 600
Qy 601 GCCCAGCTGATGCTCCCAACCGGAGCGGTAAAGACCAAGTCCCGGCGCATPACGA 660
Db 601 GCCCAGCTGATGCTCCCAACCGGAGCGGTAAAGACCAAGTCCCGGCGCATPACGA 660
Qy 661 GCTCAGGCTACCAAGTGTGTGCTCAACCCCTCGTGTGCAACAAATGAGCTTTGTGT 720
Db 661 GCTCAGGCTACCAAGTGTGTGCTCAACCCCTCGTGTGCAACAAATGAGCTTTGTGT 720
Qy 721 GCTTACATGTCCAAAGGCCATGAGATTGATCTTAATCAGAGACTGTGGGTGAGCAAT 780
Db 721 GCTTACATGTCCAAAGGCCATGAGATTGATCTTAATCAGAGACTGTGGGTGAGCAAT 780
Qy 781 ACTACTGAGGCGGATGACGATTCACACTTACAGGCAAGTTCCTTGCGGACGCGGAGTGT 840
Db 781 ACTACTGAGGCGGATGACGATTCACACTTACAGGCAAGTTCCTTGCGGACGCGGAGTGT 840
Qy 841 TCAGGAGGAGTCTTATGACATATAATTTGTGACGAGTGCACCTCCAGATGCAATCC 900
Db 841 TCAGGAGGAGTCTTATGACATATAATTTGTGACGAGTGCACCTCCAGATGCAATCC 900
Qy 901 ATCTTGGGCTATGGACATGTCTCTTGAACAGAGAGACCGCGGAGGCGAGCTGTG 960
Db 901 ATCTTGGGCTATGGACATGTCTCTTGAACAGAGAGACCGCGGAGGCGAGCTGTG 960
Qy 961 CTGCGCACCGGCTACCCCTCCGAGGCTCCGTCACGTGCGCCCATCTTAACATGAGAGT 1020
Db 961 CTGCGCACCGGCTACCCCTCCGAGGCTCCGTCACGTGCGCCCATCTTAACATGAGAGT 1020
Qy 1021 GCTCTGTCCACTTACCGGAGAGATCCCTTTATGCGCAAGCTATTCCCTTGAAGCAAT 1080
Db 1021 GCTCTGTCCACTTACCGGAGAGATCCCTTTATGCGCAAGCTATTCCCTTGAAGCAAT 1080
Qy 1081 AAGGGGGGAGACATCTCATCTTCTGCACTCAAAAGAAAGTGTGAGAGAGTGTGCGCG 1140
Db 1081 AAGGGGGGAGACATCTCATCTTCTGCACTCAAAAGAAAGTGTGAGAGAGTGTGCGCG 1140
Qy 1141 AAATGTGTGCGGTTGAGGAGTCAATGCGGAGTCTCAACGGGCTTGTGATGTCCGTC 1200
Db 1141 AAATGTGTGCGGTTGAGGAGTCAATGCGGAGTCTCAACGGGCTTGTGATGTCCGTC 1200
Qy 1201 ATCCGACCAAGTGTGAGCTGTGTGTGCTGTGCACTGACGCGCTCATGACCGGCTTTACC 1260
Db 1201 ATCCGACCAAGTGTGAGCTGTGTGTGCTGTGCACTGACGCGCTCATGACCGGCTTTACC 1260
Qy 1261 GCGCATCTTGATCGGTGATGACCTGCAACAGTGTGTCAACCAAGACATGCACTTACG 1320
Db 1261 GCGCATCTTGATCGGTGATGACCTGCAACAGTGTGTGTCAACCAAGACATGCACTTACG 1320
Qy 1261 GCGCATCTTGATCGGTGATGACCTGCAACAGTGTGTGTCAACCAAGACATGCACTTACG 1320
Db 1261 GCGCATCTTGATCGGTGATGACCTGCAACAGTGTGTGTCAACCAAGACATGCACTTACG 1320
Qy 1321 CTGACCCCTACCTTACCATGAGCAATCAAGTGTGCTCCAGAGTGTGTCTCCGTA 1380
Db 1321 CTGACCCCTACCTTACCATGAGCAATCAAGTGTGCTCCAGAGTGTGTCTCCGTA 1380
Qy 1381 CAAAGTGTGAGGAGTGTGAGCTGTGCAAGAGGAAACCAAGCATCTTACAGATTTGTG 1440
Db 1381 CAAAGTGTGAGGAGTGTGAGCTGTGCAAGAGGAAACCAAGCATCTTACAGATTTGTG 1440
Qy 1441 GAGGCTCTTCTGTGAGTGTGATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1500
Db 1441 GAGGCTCTTCTGTGAGTGTGATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1500
Qy 1501 GCTTGTATGAGCTTACCGCGCGGAGCAACAGTTAGGCTTACGAGCATATGAACACC 1560
Db 1501 GCTTGTATGAGCTTACCGCGCGGAGCAACAGTTAGGCTTACGAGCATATGAACACC 1560
Qy 1561 CCGGACTTCCCGTGTGCAAGACCATCTTGAATTTTGGAGGAGGCTTTTACCGGCTCTC 1620

Db 1561 CCGGACCTTCCCGTGTGCGCAAGACCATCTGAAATTTTGGAGGCGCTTTTACGGGTCTC 1620
Qy 1621 ACCCATATGAGAGCCCATCTTCTATCCAGACAAAGCAGAGTGGGAAAACCTTCCCTAT 1680
Db 1621 ACCCATATGAGAGCCCATCTTCTATCCAGACAAAGCAGAGTGGGAAAACCTTCCCTAT 1680
Qy 1681 CTGGTAGGCTACCAAGCCACCGTGTGCGTAGAGCTCAAGCCCTCCCGCTGTGGAGC 1740
Db 1681 CTGGTAGGCTACCAAGCCACCGTGTGCGTAGAGCTCAAGCCCTCCCGCTGTGGAGC 1740
Qy 1741 CAGATGTGAAAGTCTTATCCGTCTCAAGCCACCTTCATGAGGCAACCTTGTCTA 1800
Db 1741 CAGATGTGAAAGTCTTATCCGTCTCAAGCCACCTTCATGAGGCAACCTTGTCTA 1800
Qy 1801 TATATACCTGGGCGCTGTCCAGATGATGACCTTGAGCCAGTCAACCAAGTATATC 1860
Db 1801 TATATACCTGGGCGCTGTCCAGATGATGACCTTGAGCCAGTCAACCAAGTATATC 1860
Qy 1861 ATGACATGATATGCTGGCTGACCTGAGAGTCTCAAGAGTACCTGGAGTCTGTGGCGGC 1920
Db 1861 ATGACATGATATGCTGGCTGACCTGAGAGTCTCAAGAGTACCTGGAGTCTGTGGCGGC 1920
Qy 1921 GTTCTGCTGCTTTTGGCGCGGATTTGCTTATCCAGAGCTGTGCTCATAGTAGTAG 1980
Db 1921 GTTCTGCTGCTTTTGGCGCGGATTTGCTTATCCAGAGCTGTGCTCATAGTAGTAG 1980
Qy 1981 ATTGCTTGTCTGGGAAAGCCGCAATCATACCCGACAGGAGTCTCTTACCGGAGTTTC 2040
Db 1981 ATTGCTTGTCTGGGAAAGCCGCAATCATACCCGACAGGAGTCTCTTACCGGAGTTTC 2040
Qy 2041 GATGAATGGAAGAGTGCTGA 2061
Db 2041 GATGAATGGAAGAGTGCTGA 2061

RESULT 7

US-09-721-479B-6

Sequence 6, Application US/09721479B

GENERAL INFORMATION:

APPLICANT: Colt, Doris

APPLICANT: Medina-Selby, Angelica

APPLICANT: Selby, Mark

APPLICANT: Houghton, Michael

TITLE OF INVENTION: NOVEL HCV NON-STRUCTURAL POLYPEPTIDE

FILE REFERENCE: PP01617.002

CURRENT APPLICATION NUMBER: US/09/721,479B

NUMBER OF SEQ ID NOS: 19

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 6

LENGTH: 6299

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: pns34a

NAME/KEY: CDS

LOCATION: (1990)..(4047)

US-09-721-479B-6

Query Match 86.7%; Score 1787; DB 31; Length 6299;
Best Local Similarity 91.7%; Pred. No. 0;
Matches 1889; Conservative 0; Mismatches 170; Indels 0; Gaps 0;

Qy 1 ATGGGCGCTATACGGGCTTATGCCAGACAGACAGAGGCGCTTTGGAGTGCATATACCC 60
Db 1990 ATGGGCGCCATACGGGCGCTATGCCAGACAGACAGAGGCGCTCTCTAGGCTGCAATATACCC 2049
Qy 61 ACCTGACCGGCGCGGACAAAGACAGAGTGGAGGCTTCAATCGTGCACACTGCT 120
Db 2050 ACCCTTACTGGCGCGGACAAAGACAGAGTGGAGGCTTCAATCGTGCACACTGCT 2109
Qy 121 GCCGACACTTCTTGGCAACTGCAATTAAGGGGCTGTGGACTGTCTACCATGAGGCC 180
Db 121 GCCGACACTTCTTGGCAACTGCAATTAAGGGGCTGTGGACTGTCTACCATGAGGCC 180

Db 2110 GCCCAACCTTCTTGCGCAAGTGCATCAATGGGCTGTGCTGAGACTGTCTACCAAGCGGCGC 2169
Qy 181 GGAACAGAGCACTTGGCTACCTTAAGGCTCTGTTATCCAGATGATACCAATGTGAGC 240
Db 2170 GGAACAGAGCACTTGGCTACCTTACCGGCTCTGTTATCCAGATGATACCAATGTGAGC 2229
Qy 241 CAAGACTCTGATAGCTGCGCCGCTCCCGAAGGTGCGCTCATTTAAACATGACACTTGC 300
Db 2230 CAAGACTCTGATAGCTGCGCCGCTTCCGAGGTACCGGCTCATTTAAACATGACACTTGC 2289
Qy 301 GACTCTTGAGACTTTCATCTGTGTCAGAGGCAAGCGGATTCATCTTCTGTCGCGGAGCG 360
Db 2290 GACTCTTGAGACTTTCATCTGTGTCAGAGGCAAGCGGATTCATCTTCTGTCGCGGAGCG 2349
Qy 361 GGTATGACAGGGGAGGCTGCTTGGCGCGGCTTATCTGTTATGTAAGGCTCTGCG 420
Db 2350 GGTATGACAGGGGAGGCTGCTGTCGCGCGGCTTATCTGTTATGTAAGGCTCTGCG 2409
Qy 421 GGAGGCGCTCTGCTGTCGCGGCAAGATGCGGTAGGCAATTCAGAGCCGCGGTATGC 480
Db 2410 GGAGGCGCTCTGCTGTCGCGGCAAGATGCGGTAGGCAATTCAGAGCCGCGGTATGC 2469
Qy 481 ACCGCTGAGTGGCTTAAGCGGCTGAGCTTATCCCGTATGAGAGCTTATGAGCAACATG 540
Db 2470 ACCGCTGAGTGGCTTAAGCGGCTGAGCTTATCCCGTATGAGAGCTTATGAGCAACATG 2529
Qy 541 AGGTCCCGGCTTCTCAGACAACTCTCCGACAGAGTGGCGGACGCTTACCAAGT 600
Db 2530 AGGTCCCGGCTTCTCAGACAACTCTCTCCGACAGAGTGGCGGACGCTTACCAAGT 2589
Qy 601 GCCCACTGCAATCTCCACCGCGGAGCGGTAAAGACCAAGAGTCCCGGCGCATACGCA 660
Db 2590 GCTCACCTCCAGTCTCCACAGGAGCGGCAAAACCAAGAGTCCCGGCGCATATGCA 2649
Qy 661 GCTCAGGCTTACAGAGTGTGCTCAACCCCTCGTGTGCTGCAACAATGGGCTTTGCT 720
Db 2650 GCTCAGGCTTATTAAGTGTGCTTACTCAACCCCTCGTGTGCTGCAACAATGGGCTTTGCT 2709
Qy 721 GCTTACATGTCGAAGGCGGATGATGATCTTACATCAGGACGAGGAGTGAACAAT 780
Db 2710 GCTTACATGTCGAAGGCGGATGATGATCTTACATCAGGACGAGGAGTGAACAAT 2769
Qy 781 ACTACTGCGAGCGCGCATGATTCACCTTACGCGCAAGTCTCTTCCGACCGCGGCTGT 840
Db 2770 ACCACTGCGAGCGCGCATGATTCACCTTACGCGCAAGTCTCTTCCGACCGCGGCTGT 2829
Qy 841 TCAGGCGGCTTATGACATAATTAATTTGTGACGAGTGCCTTCCAGGATGCAACATGC 900
Db 2830 TCAGGCGGCTTATGACATAATTAATTTGTGACGAGTGCCTTCCAGGATGCAACATGC 2889
Qy 901 ATCTTGGGCTATGGAATGTCCTTGAACAAGACCGCGGGCGAGACTGACTGTG 960
Db 2890 ATCTTGGGCTATGGAATGTCCTTGAACAAGACCGCGGGCGAGACTGACTGTG 2949
Qy 961 CTGCGCACCGTACCCCTCCGCGCTCCGTCATCTGTCGCCCATCTTAACATGAGAGGTT 1020
Db 2950 CTGCGCACCGTACCCCTCCGCGCTCCGTCATCTGTCGCCCATCTTAACATGAGAGGTT 3009
Qy 1021 GCTCTGTCCACTACCGGAGATGCCCTTTATGCGAAGGCTATTCCTCTTAAGCAATT 1080
Db 3010 GCTCTGTCCACTACCGGAGATGCCCTTTATGCGAAGGCTATTCCTCTTAAGCAATT 3069
Qy 1081 AAGGGGGGAGCATCTCATCTTTCGCACTAAAGAAAGTGGAGGAGTCCCGGCA 1140
Db 3070 AAGGGGGGAGCATCTCATCTTTCGCACTAAAGAAAGTGGAGGAGTCCCGGCA 3129
Qy 1141 AAATGTGTGCGGCTTGGGCTGATGCGGTGCTTACTACCGGCGCTTGTATGTCCGTC 1200
Db 3130 AAATGTGTGCGGCTTGGGCTGATGCGGTGCTTACTACCGGCGCTTGTATGTCCGTC 3189
Qy 1201 ATCCGACCAAGTGTGAGCTGTGTGCTGTGCACTGACGCGCTTATGACCGGCTTATAC 1260
Db 3190 ATCCGACCAAGTGTGAGCTGTGTGCTGTGCACTGACGCGCTTATGACCGGCTTATAC 3249

Db 2830 TCGGGGGGGCTTATGACATATTAATTTGTGACGAGTGCACCTCCACGGATGCCACATCC 2889
Qy 901 ATCTTGGGATTTGGCACTCTCTCTTGAACCAAGAGAGACCGGGGGGGGAGACTGACTG 960
Db 2890 ATCTTGGGATTTGGCACTCTCTCTTGAACCAAGAGAGAGACCGGGGGGGGAGACTGACTG 2949
Qy 961 CTGCGCACCGCTACCCCTCCGGGCTCCGTCATGTCGCCCATCTTAACATCGAGAGAGTT 1020
Db 2950 CTGCGCACCGCACCCCTCCGGGCTCCGTCATGTCGCCCATCTTAACATCGAGAGAGTT 3009
Qy 1021 GCTCTGTCCACTACCGGAGAGATCCCTTTTATGCGAAGGCTATTCCTTGAAGCAAT 1080
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Qy 1081 AAGGGGGGAGACATCTCATCTTCTGCCACTCAAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
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Db 3130 AAGCTGTGTGCGATTTGGGCAATGCGCGGCTTACTACCGGGGCTTGAATGTCCGTC 3189
Qy 1201 ATCCGACCAAGTGTGACGTTGTGTGTGCACTGACGCGCTCATGACCGGCTTTTACC 1260
Db 3190 ATCCGACCAAGGCGGAGATGTTGTGTGTGTGCACTGACGCGGCTTGAATGTCCGTC 3249
Qy 1261 GCGGACTTGTGATTCGGTGTATGACCTGCAACAGTGTGTGACCGGAGAGAGAGAGAG 1320
Db 3250 GCGGACTTGTGATTCGGTGTATGACCTGCAATGCGTGTGTGACCGGAGAGAGAGAGAG 3309
Qy 1321 CTGACCCCTACCTTACCACTTGAACATCAAGCTTCCCGAGAGAGAGAGAGAGAGAGAG 1380
Db 3310 CTGACCCCTACCTTACCACTTGAACATCAAGCTTCCCGAGAGAGAGAGAGAGAGAGAG 3369
Qy 1381 CAACGTCGGGGGTAGACCTGCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
Db 3370 CAACGTCGGGGGTAGACCTGCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3429
Qy 1441 GAGGCTCTTCTGCGCATTTTGAATCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 1500
Db 3430 GAGGCTCTTCTGCGCATTTTGAATCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 3489
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Qy 1561 CCGGACTTCCCGTGTGCGAAGACCATCTTGAATTTTGGAGGGGCTTTTACGGGCTTC 1620
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Qy 1621 ACCCATATGACGCCCATCTTCTATCTCCAGACAAAGACAGAGTGGGAGAAACCTTCTAT 1680
Db 3610 ACTCATATATGAGGCCCATCTTCTATCTCCAGACAAAGACAGAGTGGGAGAAACCTTCTAT 3669
Qy 1681 CTGTAAGGTAACCAAGCAACGCTGTGCTAGAGCTCAAGCCCTCCCGGTGGGAGAC 1740
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Qy 1801 TATAGACTGGGCGCTGTCCAAATAGTACCTTGAAGGACCCAGTCAACCAATATATC 1860
Db 3790 TACACACTGGGCGCTGTCCAAATAGTACCTTGAAGGACCCAGTCAACCAATATATC 3849
Qy 1861 ATGACATGATGTGGGCTGACCTGAGAGGCTCAAGAGTACTGGGTGTCTTGGGCGGC 1920
Db 3850 ATGACATGATGTGGGCTGACCTGAGAGGCTGACAGAGCACTGGGCTGTCTTGGGCGGC 3909
Qy 1921 GTTCTGTGCTTTGGCGCGCTATGCTATCCAGAGCTGCTGTCTATAGTATAGG 1980

Db 3910 GTCTGTGCTTTTGGCGCGCTATGCTGTCAACAGAGCTGCTGTATAGTGGGACAG 3969
Qy 1981 ATGTCTGTCCGGAAGCGCGCATATACCCGACAGGAGAGTCTTACCGGAGATTC 2040
Db 3970 GTGCTTGTCCGGAAGCGCGCATATACCCGACAGGAGAGTCTTACCGAGATTC 4029
Qy 2041 GATGAATGGAAGAGTGTCT 2059
Db 4030 GATGAGATGGAAGAGTGTCT 4048

RESULT 9
US-08-403-590B-74
; Sequence 74, Application US/08403590B
; GENERAL INFORMATION:
; APPLICANT: Chien, David Y.
; APPLICANT: Rutler, William J.
; TITLE OF INVENTION: NANBV Diagnostics and Vaccines
; NUMBER OF SEQUENCES: 777
; CORRESPONDENCE ADDRESS:
; ADDRESS: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608-2916
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,590B
; FILING DATE: 14-MAR-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Hardin, Alisa A.
; REGISTRATION NUMBER: 33,895
; REFERENCE/DOCKET NUMBER: 0110.002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508)359-3885
; TELEFAX: (508)359-3876
; INFORMATION FOR SEQ ID NO: 74:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7310 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 3..7310
US-08-403-590B-74

Query Match 86.7% Score 1786; DB 14; Length 7310;
Best Local Similarity 91.7% Pred No 0; Mismatches 170; Indels 0; Gaps 0;
Matches 1888; Conservative 0;

Qy 2 TGGCGCTATACCGGCTATGCGCGAGACAGAGGGGCTTTTGGAGTATGATATACCA 61
Db 1729 TGGCGCTATACCGGCTATGCGCGAGACAGAGGGGCTTTTGGAGTATGATATACCA 1788
Qy 62 GTTTACCGGCGGAGACAAACCAAGTGTGAGAGGTTCAATGCTGTCAACTGTCTG 121
Db 1789 GCTTACCTGCGCGGAGACAAACCAAGTGTGAGAGGTTCAATGCTGTCAACTGTCTG 1848
Qy 122 CCCAGACTTCTTGGCACTGCAATTAACGGGCTGTGTGACTGTCTACCATGAGCGG 181
Db 1849 CCCAATCTTCTGCAACGTCATCAATGAGGCTGTGTGACTGTCTACCATGAGCGG 1908
Qy 182 GAACAGAGACCATGCTGACCTTAAGGCTCTGTATTCAGATGTACCAATGTGACC 241
Db 1909 GAACAGAGACCATGCTGACCTTAAGGCTCTGTATTCAGATGTATACCAATGTGACC 1968

QY 242 AAGACCTGTAGGCTGGCCCGCTCCCAAGGTCGCCCTCATTAACACCATGCACTTGG 301
Db 1969 AAGACCTGTAGGCTGGCCCGCTCCCAAGGTCGCCCTCATTAACACCATGCACTTGG 2028
QY 302 GCTCTCGGACCTTTAAGCTGTGCAAGGAGCAGCGATGCTATTCCTGTGCGCCGAGCG 361
Db 2029 GCTCTCGGACCTTTAAGCTGTGCAAGGAGCAGCGATGCTATTCCTGTGCGCCGAGCG 2088
QY 362 GTGATGGCAGGAGCAGCTGTGCTTTGCGCCCGCTATCTTACTTGAAGGCTCTCTGG 421
Db 2089 GTGATGGCAGGAGCAGCTGTGCTTTGCGCCCGCTATCTTACTTGAAGGCTCTCTGG 2148
QY 422 GAGGCTCTGTGCTGTGCGCCCGAGAGCATGCGGATGGCATATTGAGAGCGCGGTATGA 481
Db 2149 GAGGCTCTGTGCTGTGCGCCCGAGAGCATGCGGATGGCATATTGAGAGCGCGGTATGA 2208
QY 482 CCCGTGAGTGGCTAAGCGGTGCACTTTCATCCCGTAGAGACTTAGAGCAACATGA 541
Db 2209 CCCGTGAGTGGCTAAGCGGTGCACTTTCATCCCGTAGAGACTTAGAGCAACATGA 2268
QY 542 GGTCCCGGTGTTCTCAGACAACTCTCTCCCAAGAGTGCCTCCAGACTTCAAGTGG 601
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QY 602 CCCACTGATGCTCCCAAGCGGAGGTAAGAGACCAAGGTCGCCGCGGATACGAG 661
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QY 662 CTCAGGAGCTAAGGCTGTGCTCAACCCCTCCGTCTGCAACATGAGGCTTGTGG 721
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QY 722 CTTAACATGCTCAAGGCTGAGATGATCTTCAATCATCAGACTGAGGCTGAGCAATTA 781
Db 2449 CTTAACATGCTCAAGGCTGAGATGATCTTCAATCATCAGACTGAGGCTGAGCAATTA 2508
QY 782 CTACCTGGAGCCCGATCAGATATTCACCTAAGGAGTTCCTTCCGAGCGCGGTGT 841
Db 2509 CTACCTGGAGCCCGATCAGATATTCACCTAAGGAGTTCCTTCCGAGCGCGGTGT 2568
QY 842 CAGGAGGCTGTATGACATATTAATTGAGAGAGTGCATCTCAAGTGCATCA 901
Db 2569 CAGGAGGCTGTATGACATATTAATTGAGAGAGTGCATCTCAAGTGCATCA 2628
QY 902 TCTTGGGCAATTGACATGCTGTGCAAGAGCAGAGCGCGGAGGAGCTGACTGTGC 961
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QY 962 TCGCCACCGCTACCCCTCGGAGCTCCGTACATGTCGCCCATCTTAACTGAGAGGTTG 1021
Db 2689 TCGCCACCGCTACCCCTCGGAGCTCCGTACATGTCGCCCATCTTAACTGAGAGGTTG 2748
QY 1022 CTCTGTCACTACCGAGAGATCCCTTTTATGCAAGGCTATTCCTCTGGAACAATTA 1081
Db 2749 CTCTGTCACTACCGAGAGATCCCTTTTATGCAAGGCTATTCCTCTGGAAGATTA 2808
QY 1082 AAGGAGGAGACATCTCATCTTGTGCACTCAAGAAAGTGCAGAGCTGCGCGCA 1141
Db 2809 AAGGAGGAGACATCTCATCTTGTGCACTCAAGAAAGTGCAGAGCTGCGCGCA 2868
QY 1142 AACTGTGCGGTGGCGCTCAATGCGGTGCTTAACTGAGCGCGCTGATGTGCTGCTA 1201
Db 2869 AACTGTGCGGTGGCGCTCAATGCGGTGCTTAACTGAGCGCGCTGATGTGCTGCTA 2928
QY 1202 TCCCGACAGTGTGAGCTTGTGCTGTGAGCACTGACCGCTCATGACCGGCTTAAACG 1261
Db 2929 TCCCGACAGTGTGAGCTTGTGCTGTGAGCACTGACCGCTCATGACCGGCTTAAACG 2988
QY 1262 GCGACTTGTGATGATGAGCTGCAACGCTGTGCTCAACGAGAGCTTCAAGC 1321
Db 2989 GCGACTTGTGATGATGAGCTGCAACGCTGTGCTCAACGAGAGCTTCAAGC 3048

QY 1322 TTGACCTACCTTACCATTTGAGACATACAGCTTCCCAAGGATGCTGTCTCCGTAATC 1381
Db 3049 TTGACCTACCTTACCATTTGAGACATACAGCTTCCCAAGGATGCTGTCTCCGTAATC 3108
QY 1382 AACGTGCGGAGTGAAGCTGAGAGGAGGAGCCAGGATCTACAGATTTGTGAGCCGAGG 1441
Db 3109 AACGTGCGGAGTGAAGCTGAGAGGAGGAGCCAGGATCTACAGATTTGTGAGCCGAGG 3168
QY 1442 AGCGTCTTCTGAGCATGTTTGAATGCTGTGCTCTGAGAGTGTGATGACGCGGTTGG 1501
Db 3169 AGCGTCTTCTGAGCATGTTTGAATGCTGTGCTCTGAGAGTGTGATGACGAGGCTGG 3228
QY 1502 CTGTGATGAGCTTACGCGCGCGAGAGCAAGTAAAGCTAACAGATCATGAACACC 1561
Db 3229 CTGTGATGAGCTTACGCGCGCGAGAGCAAGTAAAGCTAACAGATCATGAACACC 3288
QY 1562 CGGACCTTCCGCTGTGCAAGACATCTTGAATTTTGGAGGCGCTTTTACGAGTCTGA 1621
Db 3289 CGGACCTTCCGCTGTGCAAGACATCTTGAATTTTGGAGGCGCTTTTACGAGGCTGA 3348
QY 1622 CCCATATGAGGCGCATCTTCTTATCCAGACAAAGAGTGGGAAAACTTCCCTATC 1681
Db 3349 CCCATATGAGGCGCATCTTCTTATCCAGACAAAGAGTGGGAAAACTTCCCTATC 3408
QY 1682 TGTAGCGTACCAAGCCAGCGGTGCTAGAGCTCAAGCCCTCCCGCTGTGAGGACC 1741
Db 3409 TGTAGCGTACCAAGCCAGCGGTGCTAGAGCTCAAGCCCTCCCGCTGTGAGGACC 3468
QY 1742 AGATGTGAAGTGTGATTCGCTCTCAAGCCCATCTCATAGGAGCAACCTCTGTAT 1801
Db 3469 AGATGTGAAGTGTGATTCGCTCTCAAGCCCATCTCATAGGAGCAACCTCTGTAT 3528
QY 1802 ATGAGCTGGGCTGTCCAGAAATGAATGACCTCTTACGCAACCACTGATATATTA 1861
Db 3529 ATGAGCTGGGCTGTCCAGAAATGAATGACCTCTTACGCAACCACTGATATATTA 3588
QY 1862 TGAATGATGTCGAGCTGAGCTGAGAGTGTGACAGATACCTGAGTGTGCTGAGCGG 1921
Db 3589 TGAATGATGTCGAGCTGAGCTGAGAGTGTGACAGATACCTGAGTGTGCTGAGCGG 3648
QY 1922 TTTGCGCTGCTTTGCGCGATTTGCTTATTCAGAGGCTGCTGTGATGATGATGAG 1981
Db 3649 TTTGCGCTGCTTTGCGCGATTTGCTTATTCAGAGGCTGCTGTGATGATGATGAG 3708
QY 1982 TTTGCTTGTCCGGAAGCGCGATCATATCCGAGAGGAGTCTCTTACCGGAGTTGG 2041
Db 3709 TTTGCTTGTCCGGAAGCGCGATCATATCCGAGAGGAGTCTCTTACCGGAGTTGG 3768
QY 2042 ATGAATGAGAGAGTGTCT 2059
Db 3769 ATGAATGAGAGAGTGTCT 3786

RESULT 10
US-08-444-112-74
; Sequence 74, Application US/08444112
; GENERAL INFORMATION:
; APPLICANT: Chien, David Y.
; APPLICANT: Rutek, William J.
; TITLE OF INVENTION: NANOV Diagnostics and Vaccines
; NUMBER OF SEQUENCES: 777
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,112
FILING DATE:
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/08/403,590
FILING DATE: 14-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Harbin, Alisa A.
REGISTRATION NUMBER: 33,895
REFERENCE/DOCKET NUMBER: 0110.002
TELEPHONE: (508) 359-3876
TELEFAX: (508) 359-3885
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
LENGTH: 7310 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 3..7310
US-08-444-112-74

Query Match      86.7%; Score 1786; DB 14; Length 7310;
Best Local Similarity 91.7%; Pred. No. 0;
Matches 1888; Conservative 0; Mismatches 170; Indels 0; Gaps 0;

QY 2 TGGCCGCTATCAGGCGCTATGCGCCAGCAGACAGAGGGGCGCTTTGGGATGATATATACCA 61
DB 1729 TGGCGCCATATCAGCGGCTACGCCGACAGACAGAGGGGCGCTTCTAGGGTGCATATATACCA 1788
QY 62 GCTTACCGCGCGGGAACAACAAAGAGTGAAGGTTGAGTTCAGTCTGTCAACTGCTG 121
DB 1789 GCTTACCTGCGCGGGAACAACAAAGTGAAGGTTGAGTTCAGTCTGTCAACTGCTG 1848
QY 122 CCCAGACTTTCTTGGCAACCTGATTAACGGGCTGTGTTGACTGTCTACATGAGACCG 181
DB 1849 CCCAAACCTTCTGCGACAGTCAATCAATGGGGTGTGCTGACTGTCTACACAGGGGCGG 1908
QY 182 GAACAGAGACATTTGGCTACCTAAGGGTCTGTTATCCAGATGTACACAAATGTGAGCC 241
DB 1909 GAACAGAGACATTCGGGTACCCAGAGGATCTGTCTATCCAGATGTATACCAATGTAGACC 1968
QY 242 AAGACCTGTAGGCTGGCCCGCTCCCAAGTGTGCGGCTCATTTAACACCATGCACTTGGC 301
DB 1969 AAGACCTGTGGGCTGGCCCGCTCCGACAGTGAAGCGCTCATTTGACACCTGCACTTGGC 2028
QY 302 GCTCTCTCGGACCTTTAAGTGTACAGAGGACAGCGGATGTCAATTCCTGTGCGCCGACGGG 361
DB 2029 GCTCTCTCGGACCTTTAAGTGTACAGAGGACAGCGGATGTCAATTCCTGTGCGCCGACGGG 2088
QY 362 GGTATGAGAGGGGAGCGCTGTTGGCCCGGCTATCTCTTAATTGAAGGCTCTCGG 421
DB 2089 GGTATGAGAGGGGAGCGCTGTTGGCCCGGCTATCTCTTAATTGAAGGCTCTCTCGG 2148
QY 422 GAGGCGCTCTGTGCTGCGCCCGAGAGCATGCGGTAGGCATATTTCAGAGCGCGGTATGCA 481
DB 2149 GAGGCGCTCTGTGCTGCGCCCGAGAGCATGCGGTAGGCATATTTCAGAGCGCGGTATGCA 2208
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DB 2209 CCCGTGAGAGTGGCTTAAGGCGGTGACTTATCCCGGTAGAGACTTTAGAGCAACCATGA 2268
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DB 2269 GGTCCCGGCTGTTCTCAGACATCTCTCTCCCAACAGAGTGCACCAAGCTCAAGTGG 2328
QY 602 CCACACTGTGATCTCCACAGCGGAGGTAGAGCAACAAAGTCCCGGCGGATACGCA 661
DB 2329 CTACACTGTGATCTCCACAGCGGAGGTAGAGCAACAAAGTCCCGGCGGATACGCA 2388
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QY 662 CTCAGGGGTCAGAGGTGCGGTCACACCCCTCCGTTGCTGCAACAATAGGCTTTGGTG 721
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DB 2449 CTTCATGTCACAGGCGCATGGGATTGATCTTAACATCAGAGACTGGGGTGAAGACAATTA 2508
QY 782 CTACTGGGAGCGCCGATTCACGTTATTCACCTTACAGGCAAGTTCTTCCGACCGGGGTGT 841
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QY 962 TCGCCACCGCTACCCCTTCGGGCTCCGTCATGTGCCCCATCTTAACATTCAGAGAGTTG 1021
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QY 1082 AGGGGGGAGACATCTCATCTTCTGCACTCAACAAAGAAAGTGCAGAGCTCGCGCA 1141
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DB 2989 GCGACTTGATTCGGGTATGACTGCAACAGCTGTGTGACCCAGACAGTGCATTCAGCC 3048
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DB 3049 TTGACCTTACTTCAACATTTAGACATTCAGCTTCCAGAGTCTGTCTCCGCTATCTC 3108
QY 1382 AACGTGCGGAGTGAAGCTGGCAGAGAGGAGCCAGGATCTTACAGATTTGTGAGACGGGGG 1441
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QY 1562 CGGGAATTCCTCGGTGCGCAAGACCATTTTGAATTTTGGAGAGGCGCTCTTTACGGGTCTCA 1621
DB 3289 CGGGAATTCCTCGGTGCGCAAGACCATTTTGAATTTTGGAGAGGCGCTCTTTACGGGCTCTCA 3348
QY 1622 CCCACATAGACGCGCACTTCTCATCCAGACCAAAAGAGTGGGGAACCTTCCCTATC 1681
DB 3349 CTCATATAGATGCCCATCTTTCTATCCAGACAAAGAGTGGGGAACCTTCCCTATC 3408
QY 1682 TGTAGCGTACCAAGCCACCGGTGCGTGAAGCTCAAGCCCTCCCGCTGTGGAGCC 1741
DB 3409 TGTAGCGTACCAAGCCACCGGTGCGTGAAGCTCAAGCCCTCCCGCTGTGGAGCC 3468
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QY 1742 AGATGTGAAGTGTGATCCGTCTCAAGCCCACTCCATGGGCAACACTCTGTCTAT 1801
| | | | |
Db 3469 AGATGTGAAGTGTGATCCGTCTCAAGCCCACTCCATGGGCAACACTCTGTCTAT 3528
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QY 1802 ATAGACTGGGCGCTGTCCAGAAATGAAGTCACTTCAACGCACTCAACCAATATATCA 1861
| | | | |
Db 3529 ACAGACTGGGCGCTGTCCAGAAATGAAGTCACTTCAACGCACTCAACCAATATATCA 3588
| | | | |
QY 1862 TGACATGTATGTCCGCTGACCTGGAGTGTGTCAACAGTATCCGTTGGCGCG 1921
| | | | |
Db 3589 TGACATGTATGTCCGCTGACCTGGAGTGTGTCAACAGTATCCGTTGGCGCG 3648
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QY 1922 TTCTGCTGTCTTGGCCCGGATTTGCTTCAACAGGCTGCTGTGATAGTAGTAGGA 1981
| | | | |
Db 3649 TTCTGCTGTCTTGGCCCGGATTTGCTTCAACAGGCTGCTGTGATAGTAGTAGGA 3708
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QY 1982 TTGCTTGTCCGGAAGCCGGCAATCATCCGCAAGGAGTCTTCAACGGAAGTTG 2041
| | | | |
Db 3709 TTGCTTGTCCGGAAGCCGGCAATCATCCGCAAGGAGTCTTCAACGGAAGTTG 3768
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QY 2042 ATGAATGGAAGAGTCT 2059
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Db 3769 ATGAATGGAAGAGTCT 3786
| | | | |

RESULT 11

US-08-436-966-1
Sequence 1, Application US/08436966
GENERAL INFORMATION:
APPLICANT: Miyamura, Tatsuo
APPLICANT: Saito, Izumi
APPLICANT: Houghton, Michael
APPLICANT: Weiner, Amy J.
APPLICANT: Han, Jang
APPLICANT: Kolberg, Janice A.
APPLICANT: Cha, Tai-An
APPLICANT: Irvine, Bruce D.
TITLE OF INVENTION: New HCV Isolates
NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,966
FILING DATE: 08-MAY-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/456,142
FILING DATE: 21-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/408,045
FILING DATE: 15-SEP-1989
ATTORNEY/AGENT INFORMATION:
NAME: Harbin, Alisa A.
REGISTRATION NUMBER: 33,895
REFERENCE/DOCKET NUMBER: 0089.007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-3274
TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 9229 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "nucleic acid"
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-436-966-1

Query Match 86.7%; Score 1786; DB 14; Length 9229;
Best Local Similarity 91.7%; Pred. No. 0;
Matches 1888; Conservative 0; Mismatches 170; Indels 0; Gaps 0;

QY 2 TGGGCTTATCAAGGCTTATGCCAGACAGAAAGGAGCTTTGGATGATATATACCA 61
| | | | |
Db 3440 TGGGCTTATCAAGGCTTATGCCAGACAGAAAGGAGCTTGGATGATATATACCA 3499
| | | | |
QY 62 GCTTGAACGGCGGGGCAAAAACCAAGTGTAGAGGTGTGATGATGATGATGATGAT 121
| | | | |
Db 3500 GCTTGAACGGCGGGGCAAAAACCAAGTGTAGAGGTGTGATGATGATGATGATGAT 3559
| | | | |
QY 122 CCCAGACTTCTTGGCAACTGTACATTAAGGGGATGTGATGATGATGATGATGATGAT 181
| | | | |
Db 3560 CCCAGACTTCTTGGCAACTGTACATTAAGGGGATGTGATGATGATGATGATGATGAT 3619
| | | | |
QY 182 GAAAGAGACCATTTGCTGACCTTAAGGGTCTGTTATCAAGTGTACCAATGTGACC 241
| | | | |
Db 3620 GAAAGAGACCATTTGCTGACCTTAAGGGTCTGTTATCAAGTGTACCAATGTGACC 3679
| | | | |
QY 242 AAGACTGTGTAGGCTGTGCGGCTCCCAAGGTGCGGCTCATTAACCATGATGATG 301
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 RESULT 12
 US-07-722-489-497
 Sequence 497, Application US/07722489
 GENERAL INFORMATION:
 APPLICANT: Chien, David Y.
 APPLICANT: Rutter, William J.
 TITLE OF INVENTION: NANBV Diagnostics and Vaccines
 NUMBER OF SEQUENCES: 524
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Chiron Corporation
 STREET: 4560 Horton Street
 CITY: Emeryville
 STATE: California
 COUNTRY: USA
 ZIP: 94608
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/722,489
 FILING DATE: 19910624
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Blackburn, Robert P.
 REGISTRATION NUMBER: 30,447
 REFERENCE/DOCKET NUMBER: 0110.031
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (510) 601-2702
 TELEFAX: (510) 655-3542(2)
 INFORMATION FOR SEO ID NO: 497:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9379 Base pairs
 TYPE: NUCLEIC ACID
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US-07-722-489-457

Query Match      86.7%; Score 1786; DB 7; Length 9379;
Best Local Similarity 91.7%; Pred. No. 0;
Matches 1888; Conservative 0; Mismatches 170; Indels 0; Gaps 0;

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DB 3636 AAGACCTGTGTAGAGCTGAGCGCGCTCCCAAGGTGCGCGCTATTAAACCATGACATTGCG 3695
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QY 362 GTGATGAGCAGGGGACGCTGCTTTCGCGCGCTATCTTTACTTTAAAGGCTCTCTCG 421
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QY 1262 GCGACTTGAGCTCGGTGATGACTGCAATGCTGTGTGCACTGAAGCCCTCATGACCGGCTTTACG 1321
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QY 1382 AAAGTGGAGTGAAGCTGAGAGGAAAGCAAGGATCTTACATGATTTGTGCAACGAGG 1441
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RESULT 13
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; Sequence 1, Application PC/TUS0319834
; GENERAL INFORMATION:
; APPLICANT: STAPLETON, JACK T.
; APPLICANT: MUENSCHMANN, SABINA
; TITLE OF INVENTION: A PROTEIN THAT INTERACTS WITH LIPIDS AND
; FILE REFERENCE: IOWA:045MO
; CURRENT APPLICATION NUMBER: PCT/US03/19834
; CURRENT FILING DATE: 2003-06-24
; PRIOR APPLICATION NUMBER: 10/445,724
; PRIOR FILING DATE: 2003-05-27
; PRIOR APPLICATION NUMBER: 60/392,158
; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 9401
; TYPE: DNA
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (342)..(9374)
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Best Local Similarity 91.7%; Pred. No. 0;
Matches 1888; Conservative 0; Mismatches 170; Indels 0; Gaps 0;

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RESULT 14
US-10-445-724-1
; Sequence 1, Application US/10445724
; GENERAL INFORMATION:
; APPLICANT: STRAPLETON, JACK T.
; APPLICANT: WUENSCHMANN, SABINA
; TITLE OF INVENTION: A PROTEIN THAT INTERACTS WITH LIPIDS AND
; FILE REFERENCE: IOWA:045US
; CURRENT APPLICATION NUMBER: US/10/445,724
; CURRENT FILING DATE: 2003-05-27
; PRIOR APPLICATION NUMBER: 60/392,158
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 9401
; TYPE: DNA
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (342)..(9374)
US-10-445-724-1
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Best Local Similarity 91.7%; Pred. No. 0;

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Qy      182 GAACAAAGAGCAATGGCGCTACCTTAAGGGGTGTGATGATCTGATCAACATGAGCCG 241
Db      3598 GAACAAAGAGCAATGGCGCTACCTTAAGGGGTGTGATGATCTGATCAACATGAGCCG 3657
Qy      242 AAGACTGTAGAGTGGCGCGCTCCCAAGGTGCGGCTCAATTAACACCATGCACTTGGC 301
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Qy      482 CCGGTGAGTGAAGCGGCTGATCTTCAATCCCGTGAAGAGCTTTAGAGCAACATGA 541
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Qy      542 GGTCCCGGAGTGTCAAGCAATCTCTCCCAAGAGTGGCGGAGCTCAAGTGG 601
Db      3958 GGTCCCGGAGTGTCAAGCAATCTCTCTCCCAAGAGTGGCGGAGCTCAAGTGG 4017
Qy      602 CCCACCTGATGCTCCACCGGAGGAGTGAAGAGCAACAGTCCCGCGGATATGCGAG 661
Db      4018 CTCACCTGATGCTCCACCGGAGGAGTGAAGAGCAACAGTCCCGCGGATATGCGAG 4077
Qy      662 CTCAGGAGCTAAGGTGTGTCTCAACCCCTCGGTGTGCTCAACATGAGGCTTTGGTG 721
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Qy      902 TCTTGGGAGTGGGAGCTGTCTGTGACAAAGAGAGAGCGGGGGGAGAGCTGAGCTGTGC 961
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| Db | 1624 | GGGGTCCCGCTGTTGTGCCCCCGGGGGCACGCGGTGGGCAATTATTTAGGGCCGCGGTGTGCA | 1683 |
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| Db | 1684 | CCCGTGAAGTGGCTAAAGCCGGTGAAGCTTCATCCCGGTAGAGAGACTTAAAGACAAACCATGA | 1743 |
| QY | 542 | GGTCCCGGGTGTTCCTCAAGCAACTCTCTCCCAACGACAGTGGCCCGAGACTACCAAGTGG | 601 |
| Db | 1744 | GGTCCCGGGTGTTCAGGATTAATCTCTCTCCACAGATGGTGGCCCGAGCTTCACAGTGG | 1803 |
| QY | 602 | CCCACTTCATGTCTCCACACGGGACGGGTAAAGACCAAGGTCCCGGCCGATAGCGAG | 661 |
| Db | 1804 | CTCACCTTCATGTCTCCACAGGACGGGAAAGACCAAGGTCCCGGTGATATGCAAG | 1866 |
| QY | 662 | CTCAGGGGTACAGAGGTGGTGGTCTCAACCCCTCCGTTGCTGCACAATGGGCTTTGGTGG | 721 |
| Db | 1864 | CTCAGGGGTATTAAGGTGGTAGTACTCAACCCCTCTGTTGGTGTCAACACTGGGCTTTGGTGG | 1922 |
| QY | 722 | CTTACATGTCCAAAGGCCCATGGGGATTGATCTTAACATACGACGTGGGGTGAAGACAAATTA | 781 |
| Db | 1924 | CTTACATGTCCAAAGGCTCATGGGATTCGATCTTAAATCATGAGACCAGGGGTGAGAACAAATTA | 1983 |
| QY | 782 | CTACTGGAGAGCCCGAATCAAGTATTCACCTTAAGGGAGTGCCTTGGCCGACGGCCGGGTGT | 841 |
| Db | 1984 | CCACTGGAGAGCCCGAATCAAGTATTCACCTTAAGGGAGTGCCTTGGCCGACGGCCGGGTCT | 2043 |
| QY | 842 | CAGGGGGGTGCTTATATGACATTAATATTTGTGACGAGTGCACCTCCAGATGCACATGCA | 901 |
| Db | 2044 | CGGGGGGGGCTTATATGACATTAATATTTGTGACGAGTGCACCTCCAGATGCACATGCA | 2103 |
| QY | 902 | TCTTGGGCAATTGGCACTGTCTCTTGAACCAAGCAGAGACCGCGGGGGCGAGACTGACTGTGGC | 961 |
| Db | 2104 | TCTTGGGCAATTGGCACTGTCTCTTGAACCAAGCAGAGACTGCGGGGGCGAGACTGACTGTGGC | 2163 |
| QY | 962 | TGCGCACCGGTAAACCCCTCCGGGCTCCGTACCTGTGCCCCCATCCAAACATCGAGGGAGTTG | 1022 |
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| QY | 1022 | CTCTGTCACTACCGGAGAGATCCCTTTTATGGAGAGGCTATTCCTCTTGAAGCAATTTA | 1081 |
| Db | 2224 | CTCTGTCACTACCGGAGAGATCCCTTTTATGGAGAGGCTATTCCTCTTGAAGCAATTTA | 2283 |
| QY | 1082 | AGGGGGGGAGACATCTCATCTTCTGCACTCAAGAAGAGTGCAGCAGAGCTCGCGCAA | 1141 |
| Db | 2284 | AGGGGGGGAGACATCTCATCTTCTGCACTCAAGAAGAGTGCAGCAGAGCTCGCGCAA | 2343 |
| QY | 1142 | AACGTGTGGCGTTGGGGCGTCAATGCGGTGGCTTACTACCGCGGCTTGAATGTGTCCGTCA | 1201 |
| Db | 2344 | AGCTGTGGCAATTGGGCATCAATGCGGTGGCTTACTACCGCGGCTTGAATGTGTCCGTCA | 2403 |
| QY | 1202 | TCCGACCAAGTGGTACGTTGTCTGTGGGCAACTGACGCGCTCAATGACCGGCTTTACCG | 1261 |
| Db | 2404 | TCCGACCAAGGCGGCATGTGTGTGTGTGGCAACGATGCCCTTCAATGACCGGCTTTACCG | 2466 |
| QY | 1262 | GCGACTTCGATTCGGGTGATGACCTGCAACACGTTGTGTCAACCGACAGTGTGACTTCAGCC | 1321 |
| Db | 2464 | GCGACTTCGATTCGGGTGATGACCTGCAATACGTTGTGTCAACCGACAGTGTGACTTCAGCC | 2522 |
| QY | 1322 | TTGACCCCTTACCTTCAACATTTAGACAAATCAAGCTTCCCAAGATGCTGTCTCCGTAATC | 1381 |
| Db | 2524 | TTGACCCCTTACCTTCAACATTTAGACAAATCAAGCTTCCCAAGATGCTGTCTCCGTAATC | 2583 |
| QY | 1382 | AACGTCGGGGGTAGGACCTGGCAGAGGGAAGCAGAGGATCTACAGATTTTGGGACCGGGGG | 1441 |
| Db | 2584 | AACGTCGGGGGACGACCTGGCAGAGGGAAGCAGAGGATCTTACAGATTTTGGGACCGGGGG | 2644 |
| QY | 1442 | AGCGCTCTTCTGGCAATGTTTGACTCGTCTGTCTCTGCGAGTGCATTAACGCGGGTGTG | 1501 |
| Db | 2644 | AGCGCCCTCTCGGGCAATGTTTGACTCGTCTGTCTCTGCGAGTGCATTAACGCGAGCTGTG | 2703 |
| QY | 1502 | CTTGGTATGAGCTTAACGCCCGCGAGACCAAGTTAAGGCTACGAGCATACATGAACCC | 1561 |

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| Db | 2704 | CTTGATATGACTACACGCCGCCAGACTACAGTTTAGGCTACGAGCGTACATGAACACC | 2765 |
| Qy | 1562 | CGGGACTTCCCGTGTGCCAAGACCATCTGAAATTTTGGAGGGCGTCTTACCGGGTCTCA | 1621 |
| Db | 2764 | CGGGGCTTCCCGTGTGCCAGGACCATCTGAAATTTTGGAGGGCGTCTTACAGGCCCTCA | 2822 |
| Qy | 1622 | CCCACTATGAGGCCCATCTTCTATTCACAGACAAAGCAGAGTGGGAAACCTTCCCTATC | 1683 |
| Db | 2824 | CTCATATGAGATGCCCATCTTCTATTCACAGACAAAGCAGAGTGGGAGAACTTCCCTTAC | 2883 |
| Qy | 1682 | TGATAGCGTACCAAGCCACCGGTGTGCGGTAGGCTCAAGCCCTTCCCGGTGTGGAGC | 1741 |
| Db | 2884 | TGTATGCTACCAAGCCACCGGTGTGCGGTAGGCTCAAGCCCTTCCCGATGTGGAGC | 2944 |
| Qy | 1742 | AGATGTGAAGTGCTTGTATCCGTCTCAAGCCACCTTCATGTGGCCAAACACTTCTGAT | 1801 |
| Db | 2944 | AGATGTGAAGTGTTTGTATTCGCTCAAGCCACCTTCATGTGGCCAAACCCCTGTAT | 3003 |
| Qy | 1802 | ATTAGCTGGGCGCTGTCCAGATGATGATCACCTTGAAGCACCAGTCAACCAATATCA | 1861 |
| Db | 3004 | ACAGCTGGGCGCTGTTCAGATATAAATCACTTGAAGCACCAGTCAACCAATATCA | 3063 |
| Qy | 1862 | TGACATGATATCGCGCTGACCTGAGAGCGTCAAGATGACCTGGGTGCTGTTGGCGG | 1921 |
| Db | 3064 | TGACATGATATCGCGCTGACCTGAGAGCGTCAAGATGACCTGGGTGCTGTTGGCGG | 3122 |
| Qy | 1922 | TTCTTGAGCTTTTGGCGCGGTATTTGCCATTCACAGCGTGGGTGCTATAGTAGTAGA | 1981 |
| Db | 3124 | TCTGTGCTGCTTTTGGCGCGGTATTTGCCATTCACAGCGTGGGTGCTATAGTAGAGG | 3183 |
| Qy | 1982 | TTGTCTTGTCCGGAAAGCGGCAATCATACCGACAGGAAAGTCTCTACCGGAGTTG | 2041 |
| Db | 3184 | TGCTCTTGTCCGGAAAGCGGCAATCATCTGACAGGAAAGTCTCTACCGAGAGTTG | 3243 |
| Qy | 2042 | ATGAATATGAAGATGCT 2059 | |
| Db | 3244 | ATGAATATGAAGATGCT 3261 | |

Search completed: February 8, 2006, 01:55:09
Job time : 11529 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 7, 2006, 20:21:37 ; Search time 437 Seconds
(without alignments)
8830.487 Million cell updates/sec

Title: US-10-817-591-16

Perfect score: 2061

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3449518 seqs, 936177250 residues

Total number of hits satisfying chosen parameters: 6899036

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 1 | 1765.2 | 85.6 | 9599 | 5 | US-09-980-559A-67 |
| 2 | 1765.2 | 85.6 | 9599 | 5 | US-09-980-559B-67 |
| 3 | 1765.2 | 85.6 | 9611 | 5 | US-09-980-559A-3 |
| 4 | 1765.2 | 85.6 | 9611 | 5 | US-09-980-559A-5 |
| 5 | 1765.2 | 85.6 | 9611 | 5 | US-09-980-559A-7 |
| 6 | 1765.2 | 85.6 | 9611 | 5 | US-09-980-559A-9 |
| 7 | 1765.2 | 85.6 | 9611 | 5 | US-09-980-559B-3 |
| 8 | 1765.2 | 85.6 | 9611 | 5 | US-09-980-559B-5 |
| 9 | 1765.2 | 85.6 | 9611 | 5 | US-09-980-559B-7 |
| 10 | 1765.2 | 85.6 | 9611 | 5 | US-09-980-559B-9 |
| 11 | 1727.8 | 83.8 | 10644 | 12 | US-60-752-866-8 |
| 12 | 1727.8 | 83.8 | 11509 | 12 | US-60-752-866-2 |
| 13 | 1727.8 | 83.8 | 11509 | 12 | US-60-752-866-7 |
| 14 | 1384.4 | 67.2 | 2844 | 6 | US-10-559-431-1 |
| 15 | 1384.4 | 67.2 | 2844 | 6 | US-10-559-431-1 |
| 16 | 1379.2 | 66.9 | 8638 | 6 | US-10-686-835B-7 |
| 17 | 1379.2 | 66.9 | 8638 | 6 | US-10-686-835B-25 |
| 18 | 1379.2 | 66.9 | 8638 | 7 | US-10-686-835B-7 |
| 19 | 1379.2 | 66.9 | 8638 | 7 | US-10-686-835B-25 |
| 20 | 1379.2 | 66.9 | 8638 | 6 | US-10-686-835B-24 |
| 21 | 1379.2 | 66.9 | 8638 | 7 | US-10-686-835B-24 |

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| 22 | 1378.6 | 66.9 | 8639 | 6 | US-10-686-835B-1 | Sequence 1, Appli |
| 23 | 1378.6 | 66.9 | 8639 | 7 | US-10-686-835B-1 | Sequence 1, Appli |
| 24 | 1378.6 | 66.9 | 8643 | 6 | US-10-686-835B-4 | Sequence 4, Appli |
| 25 | 1378.6 | 66.9 | 8643 | 7 | US-10-686-835B-4 | Sequence 4, Appli |
| 26 | 1378.2 | 66.9 | 8642 | 6 | US-10-686-835B-2 | Sequence 2, Appli |
| 27 | 1378.2 | 66.9 | 8642 | 7 | US-10-686-835B-2 | Sequence 2, Appli |
| 28 | 1378 | 66.9 | 10473 | 12 | US-60-752-866-5 | Sequence 5, Appli |
| 29 | 1378 | 66.9 | 10653 | 12 | US-60-752-866-6 | Sequence 6, Appli |
| 30 | 1378 | 66.9 | 11518 | 12 | US-60-752-866-1 | Sequence 1, Appli |
| 31 | 1378 | 66.9 | 11518 | 12 | US-60-752-866-3 | Sequence 3, Appli |
| 32 | 1378 | 66.9 | 11518 | 12 | US-60-752-866-4 | Sequence 4, Appli |
| 33 | 1377 | 66.8 | 8638 | 6 | US-10-686-835B-6 | Sequence 6, Appli |
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| 35 | 1377 | 66.8 | 8648 | 6 | US-10-686-835B-5 | Sequence 5, Appli |
| 36 | 1377 | 66.8 | 8648 | 7 | US-10-686-835B-5 | Sequence 5, Appli |
| 37 | 1363.2 | 66.1 | 9595 | 6 | US-10-535-047-19 | Sequence 19, Appli |
| 38 | 1360 | 66.0 | 9596 | 5 | US-09-980-559A-69 | Sequence 69, Appli |
| 39 | 1360 | 66.0 | 9596 | 5 | US-09-980-559B-69 | Sequence 69, Appli |
| 40 | 1252 | 60.7 | 5676 | 9 | US-11-131-901-5 | Sequence 5, Appli |
| 41 | 1179.8 | 57.2 | 1899 | 6 | US-10-535-047-21 | Sequence 21, Appli |
| 42 | 1054.4 | 51.2 | 9711 | 5 | US-09-980-559A-1 | Sequence 1, Appli |
| 43 | 1054.4 | 51.2 | 9711 | 5 | US-09-980-559B-1 | Sequence 1, Appli |
| 44 | 451.6 | 21.9 | 546 | 9 | US-11-131-901-3 | Sequence 3, Appli |
| 45 | 248.6 | 12.1 | 543 | 1 | PCT-US05-35191-1 | Sequence 1, Appli |

ALIGNMENTS

RESULT 1
US-09-980-559A-67
Sequence 67, Application US/09980559A
GENERAL INFORMATION:
APPLICANT: Yamaagi, Masayuki
APPLICANT: Emerson, Suzanne
APPLICANT: Buhk, Jens
APPLICANT: Purcell, Robert
TITLE OF INVENTION: CLONED GENOME OF INFECTIOUS HEPATITIS C
TITLE OF INVENTION: CLONED GENOME OF INFECTIOUS HEPATITIS C
FILE REFERENCE: NIH255.001NP
CURRENT APPLICATION NUMBER: US/09/980.559A
CURRENT FILING DATE: 2002-05-14
PRIOR APPLICATION NUMBER: PCT/US00/15446
PRIOR FILING DATE: 2000-06-02
PRIOR APPLICATION NUMBER: US 60/137,693
PRIOR FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 70
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 67
LENGTH: 9599
TYPE: DNA
ORGANISM: Hepatitis C virus
US-09-980-559A-67
Query Match
Best Local Similarity 91.1%; Pred. No. 0;
Matches 1875; Conservative 0; Mismatches 183; Indels 0; Gaps 0;
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QY 1922 TTCTGGCTCTTGGCGCGCTATTTGCTTATCAACAGGCTGCTGTATGATGATGGA 1981
DB 5338 TTCTGGCTCTTGGCGCGCTATTTGCTTATCAACAGGCTGCTGTATGATGATGGA 5397
QY 1982 TTGTCTTGTCCGGAAGCGGCAATCATACCGAAGGGAAGTCCCTACAGGGGAGTTG 2041
DB 5398 TTGTCTTGTCCGGAAGCGGCAATCATACCGAAGGGAAGTCCCTACAGGGGAGTTG 5457
QY 2042 ATGAATGGAAGAGTGT 2059
DB 5458 ATGAATGGAAGAGTGT 5475

RESULT 2
US-09-980-559B-67
; Sequence 67, Application US/09980559B
; GENERAL INFORMATION:
; APPLICANT: Yanagi, Maaayuki
; APPLICANT: Emerson, Suzanne
; APPLICANT: Buhk, Jens
; APPLICANT: Purcell, Robert
; TITLE OF INVENTION: CLONED GENOME OF INFECTIOUS HEPATITIS C
; TITLE OF INVENTION: VIRUSES OF GENOTYPE 2a AND USES THEREOF
; FILE REFERENCE: NIH255.001NP
; CURRENT APPLICATION NUMBER: US/09/980.559B
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: PCT/US00/15446
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: US 60/137,693
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 67

LENGTH: 9599
TYPE: DNA
ORGANISM: Hepatitis C virus
US-09-980-559B-67

Query Match 85.6%; Score 1765.2; DB 5; Length 9599;
Best Local Similarity 91.1%; Pred. No. 0;
Matches 1875; Conservative 0; Mismatches 183; Indels 0; Gaps 0;

QY 2 TGGCCCTTATCAGGCTTATGCCCAGACAGACAAAGGGCTTTGGGATGCATATACCA 61
DB 3418 TGGCCCTTATCAGGCTTATGCCCAGACAGACAAAGGGCTTTGGGATGCATATACCA 3477
QY 62 GCTTACCGCGCGGACAAACCAAGGTGAGGTTCAGATCGTCAACTGCTG 121
DB 3478 GCTTACCGCGCGGACAAACCAAGGTGAGGTTCAGATCGTCAACTGCTG 3537
QY 122 CCCAGACTTTCTTGGCAACTGCAATTAACGGGATGTGGAATGTCTACATGAGCCG 181
DB 3538 CCCAGACTTTCTTGGCAACTGCAATTAACGGGATGTGGAATGTCTACATGAGCCG 3597
QY 182 GAACAAAGACCTTGGGTGCTTAAGGGTCTGTTATCCAGATGTAACCAATGTGACC 241
DB 3598 GAACAAAGACCTTGGGTGCTTAAGGGTCTGTTATCCAGATGTAACCAATGTGACC 3657
QY 242 AAGACTGTAGGCTGGCGCGCTCCCAAGTGGCGGCTATTACACCATGCACTTGGC 301
DB 3658 AAGACTGTAGGCTGGCGCGCTCCCAAGTGGCGGCTATTACACCATGCACTTGGC 3717
QY 302 GCTCTCGGACCTTTAACCCTGTCAGAGGACGCGCATGCTCATTCCTGTGCGCCGACGG 361
DB 3718 GCTCTCGGACCTTTAACCCTGTCAGAGGACGCGCATGCTCATTCCTGTGCGCCGACGG 3777
QY 362 GTGATGGCAGGGGGCAGCTGCTTTGGCCCGGCTATCTCTTAATTGAAAGCTCTCGG 421
DB 3778 GTGATGGCAGGGGGCAGCTGCTTTGGCCCGGCTATCTCTTAATTGAAAGCTCTCGG 3837
QY 422 GAGGCGCTGTGCTGTCGCGCGGACGATGCGGTAGGCAATTTAGAGCGGGATGCA 481
DB 3838 GAGGCGCTGTGCTGTCGCGCGGACGATGCGGTAGGCAATTTAGAGCGGGATGCA 3897
QY 482 CCCGTGAGTGGCTAAGGGCGGTGGAATTCATCCCGTAGAGACTTGAAGACCAATGA 541
DB 3898 CCCGTGAGTGGCTAAGGGCGGTGGAATTCATCCCGTAGAGACTTGAAGACCAATGA 3957
QY 542 GGTCCCGGTGTTCTCAGACAACTCTCCCAACAGAGTGGCCCAAGACTTACCAATGG 601
DB 3958 GGTCCCGGTGTTCTCAGACAACTCTCCCAACAGAGTGGCCCAAGACTTACCAATGG 4017
QY 602 CCCACTGTGATGCTCCCAACGGGACGGGTAAAGAGCAACAAAGTCCCGGCGGATCCGACG 661
DB 4018 CCCACTGTGATGCTCCCAACGGGACGGGTAAAGAGCAACAAAGTCCCGGCGGATCCGACG 4077
QY 662 CTACAGGGCTTACAGGTGCTGTGCTCAACCCCTCCGTGCTGCAACATAGGGCTTTGGTG 721
DB 4078 CTACAGGGCTTACAGGTGCTGTGCTCAACCCCTCCGTGCTGCAACATAGGGCTTTGGTG 4137
QY 722 CTTACATGTCAGAGGCCATGAGATTGATCTTACATCAGACTGGGGTGAAGCAATTA 781
DB 4138 CTTACATGTCAGAGGCCATGAGATTGATCTTACATCAGACTGGGGTGAAGCAATTA 4197
QY 782 CTACAGGGACGCCGATCAGTAATTCACCTACGGCAAGTTCCTTCCGACGGCGGGTGT 841
DB 4198 CTACAGGGACGCCGATCAGTAATTCACCTACGGCAAGTTCCTTCCGACGGCGGGTGT 4257
QY 842 CAGGGGGTGTCTTATGACATATATTTGTGACGAGTGCATCTCAACGATGCAATCCA 901
DB 4258 CAGGGGGTGTCTTATGACATATATTTGTGACGAGTGCATCTCAACGATGCAATCCA 4317
QY 902 TTTTGGGCAATTGGCACTGTCTTGAACAGACAGAGCCGGGGGGGAGACTGACTGTGC 961
DB 4318 TTTTGGGCAATTGGCACTGTCTTGAACAGACAGAGCCGGGGGGGAGACTGACTGTGC 4377

QY 962 TGGCACCGCTACCCCTCCGGGCTCCGTCATGTGCTCCCATCTTAACATGAGAGTTG 1021
DB 4378 TGGCACAGTGTACCCCTCCGGGCTCCGTCATGTGCTCCCATCTTAACATGAGAGTTG 4437
QY 1022 CTCTGTCCATACCGGAGAGATCCCTTTTATGCAAGGCTATTTCCCTTGAAGCAATTA 1081
DB 4438 CTCTGTCCATACCGGAGAGATCCCTTTTATGCAAGGCTATTTCCCTTGAAGGATCA 4497
QY 1082 AGGGGGGAGACATCTCCTTTCGCACTGCACTCAAAAGAGGAGCAGCAGCTGCGCA 1141
DB 4498 AGGGGGGAGACATCTCCTTTCGCACTGCACTCAAAAGAGGAGCAGCAGCTGCGCA 4557
QY 1142 AACTGTGCGCTTGGGCGTCAATGCGGTGCTTACTACCGCGGCTTGAATGTGCTGCA 1201
DB 4558 AACTGTGCGCTTGGGCGTCAATGCGGTGCTTACTACCGCGGCTTGAATGTGCTGCA 4617
QY 1202 TCCGACAGTGTGACGTTGTGTGTGCGCACTGACGCTCTCATGACCGGCTTTACG 1261
DB 4618 TCCGACAGTGTGACGTTGTGTGTGCGCACTGACGCTCTCATGACGCTTTACG 4677
QY 1262 GCGACTTGGATTCCGCTGATGACCTGCAACAGTGTGCAACCGACAGTCCGACTCAGCC 1321
DB 4678 GCGACTTGGATTCCGCTGATGACCTGCAACAGTGTGCAACCGACAGTCCGACTCAGCC 4737
QY 1322 TTGACCTTACCTTCAACATTGAGCAATCAAGCTTCCCGAGATGCTGTCCGTAATC 1381
DB 4738 TTGACCTTACCTTCAACATTGAGCAATCAAGCTTCCCGAGATGCTGTCCGTAATC 4797
QY 1382 AACGTGGGGTGAAGCTGGCAGAGGAAACGAGCATTAAGATTTGTGCAACCGGGG 1441
DB 4798 AACGTGGGGTGAAGCTGGCAGAGGAAACGAGCATTAAGATTTGTGCAACCGGGG 4857
QY 1442 AGCGTCTTCTGGGCAATGTTTGAATGCTGTGCTCTGCGAGGCTATGACGGGGTGG 1501
DB 4858 AGCGTCTTCTGGGCAATGTTTGAATGCTGTGCTCTGCGAGGCTATGACGGGGTGG 4917
QY 1502 CTTGGTATGAGCTTACGCGCGCGGACCAAGTGAAGCTACGACATCATGAACACC 1561
DB 4918 CTTGGTATGAGCTTACGCGCGCGGACCAAGTGAAGCTACGACATCATGAACACC 4977
QY 1562 CGGAACTTCCGTGTGCAAGACATCTTGAATTTTGGAGGGCTCTTACGGGTCTCA 1621
DB 4978 CGGAACTTCCGTGTGCAAGACATCTTGAATTTTGGAGGGCTCTTACGGGTCTCA 5037
QY 1622 CCCACATGACGCGCCCACTTCCATCCAGACAAACAGAGTGGGAAAACCTTCCCTATC 1681
DB 5038 CCCACATGACGCGCCCACTTCCATCCAGACAAACAGAGTGGGAAAACCTTCCCTATC 5097
QY 1682 TGGTAGCGTACCAAGCCACCGGTGCGCTGAGAGCTCAAGCCCTCCCGCTGTGGAGCC 1741
DB 5098 TGGTAGCGTACCAAGCCACCGGTGCGCTGAGAGCTCAAGCCCTCCCGCTGTGGAGCC 5157
QY 1742 AGATGTGAAGTGTGATCCGTCTCAAGCCCACTTCATGAGGCGCAACCTTGTCTAT 1801
DB 5158 AGATGTGAAGTGTGATCCGTCTCAAGCCCACTTCATGAGGCGCAACCTTGTCTAT 5217
QY 1802 ATAGACTGGGCGCTGTCCAGAAATGAAGTCAACCTTACAGCAACCAAGTCAAGTATATA 1861
DB 5218 ATAGACTGGGCGCTGTTCAGAAATGAAGTCAACCTTACAGCAACCAAGTCAAGTATATA 5277
QY 1862 TGAAGTATATGCGGCTGACCTGAGAGTCTGACAGAGTACCTGGGTGCTGTTGGCGGG 1921
DB 5278 TGAAGTATATGCGGCTGACCTGAGAGTCTGACAGAGTACCTGGGTGCTGTTGGCGGG 5337
QY 1922 TTTGGCTGTCTTGGCGCGGATTTGCTATTCACAGGCTGCGTGTCTATGATGATGAGA 1981
DB 5338 TTTGGCTGTCTTGGCGCGGATTTGCTATTCACAGGCTGCGTGTCTATGATGATGAGA 5397
QY 1982 TTTGCTGTTCGGGAAAGCGGCAATCAACCGGACAGAGGAGTCTCTTACCGGGAGTTG 2041
DB 5398 TTTGCTGTTCGGGAAAGCGGCAATTAACCGGACAGAGGAGTCTCTTACCGGGAGTTG 5457
QY 2042 ATGAATGAGAGTGTCT 2059

DB 5458 ATGAGATGGAAGAGTCT 5475

RESULT 3
US-09-980-559A-3
Sequence 3, Application US/09980559A

GENERAL INFORMATION:
APPLICANT: Yanagi, Masayuki
APPLICANT: Emerson, Suzanne
APPLICANT: Buhk, Jens
APPLICANT: Puicelli, Robert
TITLE OF INVENTION: CLONED GENOME OF INFECTIOUS HEPATITIS C
FILE REFERENCE: NIH25.001NP
CURRENT APPLICATION NUMBER: US/09/980,559A

PRIOR FILING DATE: 2002-05-14
PRIOR APPLICATION NUMBER: PCT/US00/15446
PRIOR FILING DATE: 2000-06-02
PRIOR APPLICATION NUMBER: US 60/137,693

PRIOR FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 70

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 3
LENGTH: 9611
TYPE: DNA

ORGANISM: Hepatitis C virus
US-09-980-559A-3

Query Match 85.6%; Score 1765.2; DB 5; Length 9611;
Best Local Similarity 91.1%; Pred. No. 0;
Matches 1875; Conservative 0; Mismatches 183; Indels 0; Gaps 0;

QY 2 TGGCGCTTACACGGCTTATGCCAGACAGCAAGGGGCTTTGGATCATATACCA 61
DB 3430 TGGCGCTTACACGGCTTATGCCAGACAGCAAGGGGCTTTGGATCATATACCA 3489
QY 62 GCTTGACGGGGGCAAAACCAAGGAGGTGAGGTGATGATGATGATGATGATGAT 121
DB 3490 GCTTGACGGGGGCAAAACCAAGGAGGTGAGGTGATGATGATGATGATGATGAT 3549
QY 122 CCCAGACTTCTTGACCACTGATTAAGGGGTGTGTAAGTGTGTAAGTGTGTAAGTGTG 181
DB 3550 CCCAGACTTCTTGACCACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 3609
QY 182 GAAACAAGACCATTCGCTACCTAAGGTCCTGTTATCCAGATGTAACCAATGTGACC 241
DB 3610 GAAACAAGACCATTCGCTACCTAAGGTCCTGTTATCCAGATGTAACCAATGTGACC 3669
QY 242 AAGACTGATGAGCTGCGCGCTCCCAAGGTGCGCGCTCATTAACAGATGATGATGATG 301
DB 3670 AAGACTGATGAGCTGCGCGCTCCCAAGGTGCGCGCTCATTAACAGATGATGATGATG 3729
QY 302 GCTCTCTGACCTTTTACCTGATCAGAGGACGCGCATGATGATGATGATGATGATGATG 361
DB 3730 GCTCTCTGACCTTTTACCTGATCAGAGGACGCGCATGATGATGATGATGATGATGATG 3789
QY 362 GTGATGACAGGGGACGCTGCTTGGCCCGGCTTATCTTTAATTGAAAGGCTCTCGG 421
DB 3790 GTGATGACAGGGGACGCTGCTTGGCCCGGCTTATCTTTAATTGAAAGGCTCTCTCGG 3849
QY 422 GAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 481
DB 3850 GAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3909
QY 482 CCCGTGAGTGTGTAAGGGGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 541
DB 3910 CCCGTGAGTGTGTAAGGGGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 3969
QY 542 GGTGCGCGGTGTTCTAGACACTCTCCCCACAGAGTGGCCCAAGAGTCAAGTGG 601
DB 3970 GATGCCGGGTGTTCTAGACACTCTCCCCACAGAGTGGCCCAAGAGTCAAGTGG 4029

QY 602 CCCACTGATGCTCCACCGGAGGTTAAGACCAAGGTCGGGCGGATACGACG 661
DB 4030 CCCACTGATGCTCCACCGGAGGTTAAGACCAAGGTCGGGCGGATACGACG 4089
QY 662 CTCAGGGCTAACAGGTGTGTGTCTCAACCCCTCGTTGCTGCAACAAATGGGCTTTGGTG 721
DB 4090 CTCAGGGCTAACAGGTGTGTGTGTCTCAACCCCTCGTTGCTGCAACGCTGGGCTTTGGTG 4149
QY 722 CTTCATATGCAAGGCGCCATGGATGATGATGATGATGATGATGATGATGATGATGATGAT 781
DB 4150 CTTCATATGCAAGGCGCCATGGATGATGATGATGATGATGATGATGATGATGATGATGAT 4209
QY 782 CTACTGAGAGCCGATCAAGTATTCACCTTACGCGCAATGCTTTCGACGCGGGTGT 841
DB 4210 CCACGTGAGAGCCGATCAAGTATTCACCTTACGCGCAATGCTTTCGACGCGGGTGT 4269
QY 842 CAGGGGGTCTTATGACATTAATTTGTGACAGTGTGCTCAACGATGCAATGCAATGCA 901
DB 4270 CAGAGGTGCTTATGACATTAATTTGTGACAGTGTGCTCAACGATGCAATGCAATGCA 4329
QY 902 TCTTGGGATGAGCATGCTGCTTGAACAGAGACGCGGGGGCGAGACTGTGTC 961
DB 4330 TCTTGGGATGAGCATGCTGCTTGAACAGAGACGCGGGGGCGAGACTGTGTC 4389
QY 962 TCGCACCGCTACCCCTCGGGCTCGTCACTGTGCCCATCTTAACATCGAGAGTGG 1021
DB 4390 TCGCACCGCTACCCCTCGGGCTCGTCACTGTGCCCATCTTAACATCGAGAGTGG 4449
QY 1022 CTCTGTCACTACCGGAGATGCCCTTTTATGCAAGGCTTATGCAAGGCTTATGCAAGGCT 1081
DB 4450 CTCTGTCACTACCGGAGATGCCCTTTTATGCAAGGCTTATGCAAGGCTTATGCAAGGCT 4509
QY 1082 AGGGGGGAGACATGCTCTTGTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACT 1141
DB 4510 AGGGGGGAGACATGCTCTTGTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACT 4569
QY 1142 AACTGTGCGGTGAGGCTCAATGCGGTGCTTACCTACGCGGCTTATGCTGCTGCA 1201
DB 4570 AACTGTGCGGTGAGGCTCAATGCGGTGCTTACCTACGCGGCTTATGCTGCTGCA 4629
QY 1202 TCCGACCAAGTGTGACGTTGTGCTGTGCACTGACGCGCTTATGCAAGGCTTATGCA 1261
DB 4630 TCCGACCAAGTGTGACGTTGTGCTGTGCACTGACGCGCTTATGCAAGGCTTATGCA 4689
QY 1262 GCGACTTGAATCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1321
DB 4690 GCGACTTGAATCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4749
QY 1322 TTGACCTTACCTTACCAATGAGACATGACGCTTCCAGAGATGCTGCTCCGATCTC 1381
DB 4750 TTGACCTTACCTTACCAATGAGACATGACGCTTCCAGAGATGCTGCTCCGATCTC 4809
QY 1382 AAAGTGGGGTGAAGCTGCGAGAGGAAACGAGCATCTTACAGATTTGTGCAACGGGGG 1441
DB 4810 AAAGTGGGGTGAAGCTGCGAGAGGAAACGAGCATCTTACAGATTTGTGCAACGGGGG 4869
QY 1442 AGCGTCTTCTGCGAGTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1501
DB 4870 AGCGTCTTCTGCGAGTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4929
QY 1502 CTTGGTATGAGCTTACGCGCGCGGAGACCAAGTATGAGCTATGAGCATATGACACCC 1561
DB 4930 CTTGGTATGAGCTTACGCGCGCGGAGACCAAGTATGAGCTATGAGCATATGACACCC 4989
QY 1562 CGGACCTTCCGTGTGCAAGACCATTTTGAATTTTGGAGGGGCTTTTACGGGCTTCA 1621
DB 4990 CGGACCTTCCGTGTGCAAGACCATTTTGAATTTTGGAGGGGCTTTTACGGGCTTCA 5049
QY 1622 CCCAGATGAGCGCCCATCTTCTATCCAGACCAAAAGAGTGGGGGAAACCTTCCCTATC 1681
DB 5050 CTCATATGAGTCCCATCTTCTATCCAGACCAAAAGAGTGGGGGAAACCTTCTCCCTATC 5109
QY 1682 TGGTAGCGTACCAAGCCAGTGTGCGGTAGAGTCAAGCCCTCCCGTGTGGAGCC 1741

Db 5110 TGGTAGCGTACCAAGCACCCTGTGGGCTCAAGGCTCAAGCCCTCCCATCGTGGACC 5169
Qy 1742 AGATGTGGAAGTCTTGAATCCCTCTCAAGCCACCTCTCAATGGGCCAACAACCTCTGCTAT 1801
Db 5170 AGATGTGGAAGTCTTGAATCCCTCTCAAGCCACCTCTCAATGGGCCAACAACCTCTGCTAT 5229
Qy 1802 ATAGACGTGGGCGCTGTCCAGAAATGAAGTCAACCTGTACGACCCAGTCAACAATATATCA 1861
Db 5230 ACAGACTGGGCGCTGTCCAGAAATGAAGTCAACCTGTACGACCCAGTCAACAATATATCA 5289
Qy 1862 TGACATGATATGTCCGCTGTACCTGTAGAGTGTCAACGATCACTGTGTCTGTGGCGGCG 1921
Db 5290 TGACATGATATGTCCGCTGTACCTGTAGAGTGTCAACGATCACTGTGTCTGTGGCGGCG 5349
Qy 1922 TTCTGCTGTCTTGGGCGGCTGTATGCTTATCCACAGGCTGCTGTATAGTATGATGA 1981
Db 5350 TTCTGCTGTCTTGGGCGGCTGTATGCTTATCCACAGGCTGCTGTATAGTATGATGA 5409
Qy 1982 TTGTCTGTCCGGAAGCCGGCAATCATACCGACAGGAGTCTCTACCGGGAAGTTGG 2041
Db 5410 TTGTCTGTCCGGAAGCCGGCAATCATACCGACAGGAGTCTCTACCGGGAAGTTGG 5469
Qy 2042 ATGAATGGAAGAGTGTCT 2059
Db 5470 ATGAATGGAAGAGTGTCT 5487

RESULT 4
US-09-980-559A-5
/ Sequence 5, Application US/09980559A
/ GENERAL INFORMATION:
/ APPLICANT: Yanagi, Masayuki
/ APPLICANT: Emerson, Suzanne
/ APPLICANT: Buhn, Jens
/ APPLICANT: Purcell, Robert
/ TITLE OF INVENTION: CLONED GENOME OF INFECTIOUS HEPATITIS C
/ FILE REFERENCE: NIH25.001NP
/ CURRENT APPLICATION NUMBER: US/09/980,559A
/ CURRENT FILING DATE: 2002-05-14
/ PRIOR APPLICATION NUMBER: PCT/US00/15446
/ PRIOR FILING DATE: 2000-06-02
/ PRIOR APPLICATION NUMBER: US 60/137,693
/ PRIOR FILING DATE: 1999-06-04
/ NUMBER OF SEQ ID NOS: 70
/ SOFTWARE: FaalSeQ for Windows Version 4.0
/ SEQ ID NO 5
/ TYPE: DNA
/ ORGANISM: Hepatitis C virus
US-09-980-559A-5

Query Match 85.6%; Score 1765.2; DB 5; Length 9611;
Best Local Similarity 91.1%; Pred. No. 0;
Matches 1875; Conservative 0; Mismatches 183; Indels 0; Gaps 0;

Qy 2 TGGCGCTATTCACGCGCTATGCCCAGACAGACAAAGGGGCTTTTGGAGTCATATACCA 61
Db 3430 TGGCGCTATTCACGCGCTATGCCCAGACAGACAAAGGGGCTTTTGGAGTCATATACCA 3489
Qy 62 GCTTACCGGCGGGAACAACCAAGTGAAGTGAAGTTCAGATCGGTCAACGCTG 121
Db 3490 GCTTACCGGCGGGAACAACCAAGTGAAGTGAAGTTCAGATCGGTCAACGCTG 3549
Qy 122 CCCAGACTTCTTGGCAACTGATTAACGGGGTGTGGACTGTCTACATGAGCGG 181
Db 3550 CCCAGACTTCTTGGCAACTGATTAACGGGGTGTGGACTGTCTACATGAGCGG 3609
Qy 182 GAACAAGACATTCGCTCACTAAGGGTCTGTATTCAGATGTAACCAATGTGAGC 241
Db 3610 GAACAAGACATTCGCTCACTAAGGGTCTGTATTCAGATGTAACCAATGTGAGC 3669

Qy 242 AAGACTGTAGAGTGGCCCGCTCCCAAGGTGCGCGCTCAATTAACCATGACATTGGC 301
Db 3670 AAGACTGTAGAGTGGCCCGCTCCCAAGGTGCGCGCTCAATTAACCATGACATTGGC 3729
Qy 302 GCTCTCTGGAACCTTTACTGTGTACAGAGCACCGGATGTCAATTCCTGTGGCGCGAGG 361
Db 3730 GCTCTCTGGAACCTTTACTGTGTACAGAGCACCGGATGTCAATTCCTGTGGCGCGAGG 3789
Qy 362 GTGATGGAAGGGGAGCGCTGTGGCCCGGCTATCTTACTTGAAGGCTCCTGG 421
Db 3790 GTGATGGAAGGGGAGCGCTGTGGCCCGGCTATCTTACTTGAAGGCTCCTGG 3849
Qy 422 GAGGCTCTGTGTGTGCCCCGAGAGACATGCGGTAGAGATTCAGAGCGCGATATGA 481
Db 3850 GAGGCTCTGTGTGTGCCCCGAGAGACATGCGGTAGAGATTCAGAGCGCGATATGA 3909
Qy 482 CCCGTGAGTGTCTAAGCGGTGACCTTCATCCCGTGAAGCTTGAAGACCAATGA 541
Db 3910 CCCGTGAGTGTCTAAGCGGTGACCTTCATCCCGTGAAGCTTGAAGACCAATGA 3969
Qy 542 GGTCCCGGTGTTCACAGCAATCTCTCCCAAGAGTGGCCGAGCTCAAGTGG 601
Db 3970 GATCCCGGTGTTCACAGCAATCTCTCCCAAGAGTGGCCGAGCTCAAGTGG 4029
Qy 602 CCACCTGCAATGCTCCACCGGACGCGTAAAGACCAAGGTCCCGGCGGATACGAG 661
Db 4030 CCACCTGCAATGCTCCACCGGACGCGTAAAGACCAAGGTCCCGGCGGATACGAG 4089
Qy 662 CTCAGGGCTACAGAGTGTGTGTCAACCCCTCGGTGTGTCAACATGAGGCTTTGGTG 721
Db 4090 CTCAGGGCTACAGAGTGTGTGTGTCAACCCCTCGGTGTGTCAACATGAGGCTTTGGTG 4149
Qy 722 CTTAATGTCCAAAGGCCATGGATTTGATCCTAATAGAGATGAGGAGTGAACAATTA 781
Db 4150 CTTAATGTCCAAAGGCCATGGATTTGATCCTAATAGAGATGAGGAGTGAACAATTA 4209
Qy 782 CTACTGGAAGCCGATCAAGTATTCACCTACGGAAGTTCCTTCCGAGCGGAGTGT 841
Db 4210 CTACTGGAAGCCGATCAAGTATTCACCTACGGAAGTTCCTTCCGAGCGGAGTGT 4269
Qy 842 CAGGGGCTGCTTATGACATTAATTTGTGACGAGTGTCCATCCAGATGCAATCCA 901
Db 4270 CAGGGGCTGCTTATGACATTAATTTGTGACGAGTGTCCATCCAGATGCAATCCA 4329
Qy 902 TCTTGGGATTTGGCATGTCTCTTGAACCAAGACACCGGGGGCGAGACTGATGTC 961
Db 4330 TCTTGGGATTTGGCATGTCTCTTGAACCAAGACACCGGGGGCGAGACTGATGTC 4389
Qy 962 TCGCACGCTACCCCTCGGGCTCGTCACTGTGCCCATCTTAACATCGAGAGTTG 1021
Db 4390 TCGCACGCTACCCCTCGGGCTCGTCACTGTGTCCATCTTAACATCGAGAGTTG 4449
Qy 1022 CTCTGTCACTACCGAGAGATCCCTTTTATGCAAGGCTATTCCTTGAAGCAATTA 1081
Db 4450 CTCTGTCACTACCGAGAGATCCCTTTTATGCAAGGCTATTCCTTGAAGCAATTA 4509
Qy 1082 AAGGGGGAAGACATCTCATCTTGTGCACTCAAAAGAAAGTGCAGAGCTGCGCGCA 1141
Db 4510 AAGGGGGAAGACATCTCATCTTGTGCACTCAAAAGAAAGTGCAGAGCTGCGCGCA 4569
Qy 1142 AACTGTGCGGTGTGGGCGTCAATGCGGTGTACTACCGGCGCTTGAATGTGTCGCTCA 1201
Db 4570 AACTGTGCGGTGTGGGCGTCAATGCGGTGTACTACCGGCGCTTGAATGTGTCGCTCA 4629
Qy 1202 TCCGACCAAGTGTGACGTTGTGTGTGCAATGACGCGCTCATGACCGGCTTTACG 1261
Db 4630 TCCGACCAAGTGTGACGTTGTGTGTGCAATGACGCGCTCATGACCGGCTTTACG 4689
Qy 1262 GCGACTTGTATTCGATGATACCTCAACAGTGTGTCAACCAAGTGTGCACTTCAAGC 1321
Db 4690 GCGACTTGTATTCGATGATACCTCAACAGTGTGTCACTCAAGTGTGCACTTCAAGC 4749
Qy 1322 TTGACCTTACCTTCAACATTAAGACATCAAGCTTCCGAGAGTGTCTCCGTAATC 1381

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Db 4750 TTGACCTTACCTTTTACATTTGAGACACACGCTCCCAAGATGCTGCTCAGAGACTC 4809
Qy 1382 AACGCTGGGGGTAGATTGGCAGAGGAGACCAAGCATCTACAGATTGTCACCGGGG 1441
Db 4810 AACCGCGGGGAGAGACTGGCAGGGGGAACCAAGCATCTATGATTGTCAGACCGGGG 4869
Qy 1442 AGGCTCTTCTGGCATGTTTGACTGCTGCTCTGCGAGAGTCTATGACGGGGGTG 1501
Db 4870 AGCGCCCTTCGAGCATGTTGCACTCGTCCGTCTCTGTAGTGTCTATGACGGGGCTG 4929
Qy 1502 CTGTGATGAGCTTACGCGCGCGAGACCAAGTTAGGCTACAGAGCATATGAACCC 1561
Db 4930 CTGTGATGAGCTACAGCGCGCGAGACCAAGTTAGGCTACAGAGCATATGAACCC 4989
Qy 1562 CGGAGCTTCCGCTGTGCGCAAGACATCTTGAATTTTGGAGGGCGCTTTACGGGCTCA 1621
Db 4990 CGGGGCTTCCGCTGTGCGCAAGACATCTTGAATTTTGGAGGGCGCTTTACGGGCTCA 5049
Qy 1622 CCAACATAGACGCGCACTTCTATCCGACAAAGAGAGTGGGGAAACCTTCCCTATC 1681
Db 5050 CTGATATGATGCGCATTTTATCCAGACAAAGAGAGTGGGGAAACCTTCTTACC 5109
Qy 1682 TGGTAGCTACCAAGCCACCGTGTGCTAGAGCTCAAGCCCTCCCGCTGTGGAGC 1741
Db 5110 TGGTAGCTACCAAGCCACCGTGTGCTAGAGCTCAAGCCCTCCCGCTGTGGAGC 5169
Qy 1742 AGATGGAAGTGTGATTCCTCTCAAGCCACCTTCAATGGGCCAACACTCTGCTAT 1801
Db 5170 AATGTGGAAGTGTGATTCCTCTCAAGCCACCTTCAATGGGCCAACACTCTGCTAT 5229
Qy 1802 ATAGATGGGCGGTGTCAGAAATGAAGTCAACCTGACGACCAAGTCAACAAATATATA 1861
Db 5230 AAGATGGGCGGTGTCAGAAATGAAGTCAACCTGACGACCAAGTCAACAAATATATA 5289
Qy 1862 TGAATGATGTCGAGTGAAGTGAAGTGTGTCAGAGTCAAGTGTGCTGTGGCGGCG 1921
Db 5290 TGAATGATGTCGAGTGAAGTGAAGTGTGTCAGAGTCAAGTGTGCTGTGGCGGCG 5349
Qy 1922 TTCTGCTGCTTTGGCGCGGTATGCTTATCCAGAGGCTGCTGATATGATGATGAGA 1981
Db 5350 TCTGCTGCTCTGCGCGCGGTATGCTTATCCAGAGGCTGCTGATATGATGATGAGA 5409
Qy 1982 TTGCTGTCGCGGAAAGCGGCAATCATCCGACAGAGGAGTCTCTACCGGGAGTTG 2041
Db 5410 TCGTCTGTCGCGGAAAGCGGCAATCATCTGACAGAGGAGTCTCTACCGAGGTTG 5469
Qy 2042 ATGAATGGAAGTGTCT 2059
Db 5470 ATGAGATGGAAGTGTCT 5487

RESULT 5
US-09-980-559A-7
; Sequence 7, Application US/09980559A
; GENERAL INFORMATION:
; APPLICANT: Yanagi, Masayuki
; APPLICANT: Emerson, Suzanne
; APPLICANT: Buhk, Jens
; APPLICANT: Purcell, Robert
; TITLE OF INVENTION: CLONED GENOME OF INFECTIOUS HEPATITIS C
; FILE REFERENCE: NIH25.001NP
; CURRENT APPLICATION NUMBER: US/09/980,559A
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: PCT/US00/15446
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: US 60/137,693
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FaalSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 9611
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; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-09-980-559A-7
Query Match 85.6%; Score 1765.2; DB 5; Length 9611;
Best Local Similarity 91.1%; Pred. No. 0;
Matches 1875; Conservative 0; Mismatches 183; Indels 0; Gaps 0;

Qy 2 TGGGCGCTATACAGGCGCTATGCGCCAGCAGACAGAGGGGCTTTGGAGTGCATATACCA 61
Db 3430 TGGGCGCTATACAGGCGCTATGCGCCAGCAGACAGAGGGGCTTTGGAGTGCATATACCA 3489
Qy 62 GCTTACCGGCGCGGACAAAACACAGTGAAGGTGAGATTGATGATGCTGCTG 121
Db 3490 GCTTACCGGCGCGGACAAAACACAGTGAAGGTGAGATTGATGATGCTGCTG 3549
Qy 122 CCAAGCTTCTTGGCAACCTGATTAACGGGGTGTGTTGACTGTCTACATGAGCGG 181
Db 3550 CCAAGCTTCTTGGCAACCTGATTAACGGGGTGTGTTGACTGTCTACATGAGCGG 3609
Qy 182 GAAACAGAGACATGCGCTACCTAAGGGTCTGTTATCAGATGTAACAAATGAGACC 241
Db 3610 GAAACAGAGACATGCGCTACCTAAGGGTCTGTTATCAGATGTAACAAATGAGACC 3669
Qy 242 AAGACCTGTAGGCTGCGCCGCTCCCAAGGTGCGCGCTATTAACCATGCACTTGG 301
Db 3670 AAGACCTGTAGGCTGCGCCGCTCCCAAGGTGCGCGCTATTAACCATGCACTTGG 3729
Qy 302 GCTCTGCGACCTTTTACCTGTGACAGAGGACCGCGATGTCTTCTGTGCGCGACGG 361
Db 3730 GCTCTGCGACCTTTTACCTGTGACAGAGGACCGCGATGTCTTCTGTGCGCGACGG 3789
Qy 382 GTGATGGAGGGGGGCGCTGCTTTGCGCGCGCTATCTTAAAGGCTCTGCG 421
Db 3790 GTGATGGAGGGGGGCGCTGCTTTGCGCGCGCTATCTTAAAGGCTCTGCG 3849
Qy 422 GAGGCGCTGTGTCGCGCGGACAGATGCGTGAAGATATTCAGAGCGCGGTATGCA 481
Db 3850 GAGGCGCTGTGTCGCGCGGACAGATGCGTGAAGATATTCAGAGCGCGGTATGCA 3909
Qy 482 CCGTGAAGTGTGAAGCGGTGATCTTATCCCGTGAAGACTTTAGAGCAACCATGA 541
Db 3910 CCGTGAAGTGTGAAGCGGTGATCTTATCCCGTGAAGACTTTAGAGCAACCATGA 3969
Qy 542 GGTCCCGGTGTTTCAGACAACTCTCCCAACAGAGTGCAGAGCTCAAGTGG 601
Db 3970 GATCCCGGTGTTTCAGACAACTCTCTCCCAACAGAGTGCAGAGCTCAAGTGG 4029
Qy 602 CCACTGCTATGCTCCACCGGCAAGGTGAGAGCAACAGGTCCCGGCGCATACGCA 661
Db 4030 CCACTGCTATGCTCCACCGGCAAGGTGAGAGCAACAGGTCCCGGCGCATACGCA 4089
Qy 662 CTCAGGGCTACAGGTGCTGTGCTCAACCCCTCGTGTGCTGCAACATGCGCTTTGGTG 721
Db 4090 CCAAGGGCTACAGGTGCTGTGCTCAACCCCTCGTGTGCTGCAACATGCGCTTTGGTG 4149
Qy 722 CTATATGTCGAAGGCGCATGGGATTGATCTTAATCAATGAGATGAGGAGTGAAGATTA 781
Db 4150 CTATATGTCGAAGGCGCATGGGATTGATCTTAATCAATGAGATGAGGAGTGAAGATTA 4209
Qy 782 CTACTGAGAGCCCGATCAAGTATTCACCTACGCGAAGTTCCTTCCGACGCGGGTGT 841
Db 4210 CCACTGAGAGCCCGATCAAGTATTCACCTACGCGAAGTTCCTTCCGACGCGGGTGT 4269
Qy 842 CAGGGGGTCTTATGATATTAATTTGATGAGAGTGCATCTCCAGATGCAATCTCA 901
Db 4270 CAGGGGGTCTTATGATATTAATTTGATGAGAGTGCATCTCCAGATGCAATCTCA 4329
Qy 902 TCTTGGGATGAGCATGCTGCTTGAACAGAGACAGCGCGGGGCGAGACTGATGCTG 961
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Qy 962 TCGCCACGCTACCCCTCGGGCTCGTCACTGTGCCCATCTTAACATGAGAGTGG 1021
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| | | | |
|----|------|--|------|
| Db | 4390 | TCGCACTGCTAACCCCTCCGGACCTCCGCTACCTGTCTCCATCTTAACATTCAGAGAGTTG | 4449 |
| Oy | 1022 | CTCTGTCCACTAACCGSAGAGATGCCCTTTATAGCAAGGCTATTTCCCTTGAAACAATTA | 1081 |
| Db | 4450 | CTCTGTCCACCAACCGSAGAGATCCCTTTTACGGCAAGGCTATCCCTCTGAGGTGATCA | 4509 |
| Oy | 1082 | AGGGGGGGAGACATCTCATCTTTCTGCACTCAAGAGAGAGTGGCAGAGTCCCGCA | 1141 |
| Db | 4510 | AGGGGGGGAGACATCTCATCTTTCTGCACTCAAGAGAGAGTGGCAGAGTCCCGCA | 4569 |
| Oy | 1142 | AACGTGTCCGTTGGGCGCTCAATGCCGGCTTACTACCGGGCTTGACATGTGTCCGCA | 1201 |
| Db | 4570 | AGCTGTGTGCATTTGGGCATCAATGCCGGCTTACTACCGGGCTTGACTGTCTGTGCA | 4629 |
| Oy | 1202 | TCCGACACGAGTGTACCTTTGCTCCGTGGGCAACTGACGCCCTCATGACCCGGCTTTACG | 1261 |
| Db | 4630 | TCCGACACGAGGGGCAATTTGTGTGTGTGACCGAAGCTCTCATGACTGGCTTTACG | 4689 |
| Oy | 1262 | GCGACTTGTGATTCGGTGTATGACCTGCAACAGTGTGTACCCCAAGCACTGCACTTACGC | 1321 |
| Db | 4690 | GCGACTTGTGACTGTGTATGACTGTCAACAGTGTGTACTCAAGCACTGCACTTACGC | 4749 |
| Oy | 1322 | TTGACCCCTTACCTTCAACCATTTGAGACATCAAGCTTCCCAAGATGTGTCTTCCCGTACTC | 1381 |
| Db | 4750 | TTGACCCCTTACCTTCAACCATTTGAGACACACAGCTCTCCCAAGATGTGTCTTCCAGACTC | 4809 |
| Oy | 1382 | AACGTCGGGGTATAGACTGGCAGAGGGAGACCAAGCATTAAGATTTTGTGCAACGGGGG | 1441 |
| Db | 4810 | AACGTCGGGGGCAAGACTGGCAGGGGGAGACCAAGCATTTATAGATTTTGTGCAACGGGGG | 4869 |
| Oy | 1442 | AGCGCTCTTCTGCACTGTTTGAATCTGCTGTCTTCTGCAGTGTATGACGGGGTGTG | 1501 |
| Db | 4870 | AGCGCCCTTCCGGCATGTTTGAATCTGCTGTCTTGTGAGTGTATGACCGGGGCTGTG | 4929 |
| Oy | 1502 | CTTGTGTATGACTTACGCCCGCCGAGACCAAGTTAAGCTTACAGACATACATGAACACC | 1561 |
| Db | 4930 | CTTGTGTATGACTTACGCCCGCCGAGACTTAAGTTAAGCTTACAGCGTACATGAACACC | 4989 |
| Oy | 1562 | CGGGACTTCCCGTGTGCCAAGACCATCTGAAATTTTGGAGGGGCTCTTACCGGGTCTCA | 1621 |
| Db | 4990 | CGGGCTTCCCGTGTGCCAAGACCATCTTGAATTTTGGAGGGGCTCTTACCGGGCTCTCA | 5049 |
| Oy | 1622 | CCCATATAGACGCCCACTTCTCTATCTCCAGACAAAGCAGATGTGGGAAAACCTTCCCTATC | 1681 |
| Db | 5050 | CTCATATATAGATGCCCACTTTTATCTCCAGACAAAGCAGATGTGGGAGAACTTTCCTTATC | 5109 |
| Oy | 1682 | TGTATAGCTTACCAAGCCACCGTGTGTGCTAAGACTCAAGCCCTTCCCGTGTGGAGCC | 1741 |
| Db | 5110 | TGTATAGCTTACCAAGCCACCGTGTGTGCTAAGGGCTCAAGCCCTTCCCGTGTGGAGCC | 5169 |
| Oy | 1742 | AGATGTGAAAGTCTTGAATCCGTCTCAAGGCCCAACCTCATGTGGGCAACACTCTMGCAT | 1801 |
| Db | 5170 | AGATGTGAAAGTGTGAATCCGCTTTAAACCACTTCCATGTGGCAACACCCTGCTAT | 5229 |
| Oy | 1802 | ATAGACTGGGGCTGTCTCCAGATGAAGTCACTCTGACCGCAACCAAGTCAACCAATATATCA | 1861 |
| Db | 5230 | ACAAGCTGGGGCTGTCTCAGATGAAGTCACTCTGACCGCAACCAATCAACCAATATATCA | 5289 |
| Oy | 1862 | TGACATGTATGTCCGCTGACCTGAGGTGTCTCAGAGTCACTGGGTCTGTTGGCGCG | 1921 |
| Db | 5290 | TGACATGTATGTCCGCTGACCGCTGAGGTGTCTCAGAGCACTGGGTGTCTGTTGGCGCG | 5349 |
| Oy | 1922 | TTTGTGGCTGTGGCGCGGTATTTGCCATCAAGAGTGTGGTGTATATAGGTATAGA | 1981 |
| Db | 5350 | TTCTGTGGCTGTGGCGCGGTATTTGCTCAACAGGCTGTGGTGTATATAGGTATAGA | 5409 |
| Oy | 1982 | TTGTCTTGTCCGAAAGCCGGCAATCATACCGACAGGAAAGTCTCTTACCGGGAGTTG | 2041 |
| Db | 5410 | TCGTCTTGTCCGGGAAAGCCGGCAATTAATACGTGAAGGAGGTTCTTACCAAGAGTTG | 5469 |
| Oy | 2042 | ATGAATATGAAGAGTCT 2059 | |

| | | | |
|----|------|---|------|
| Db | 5470 | ATGAGTAGGAAGACTGCT | 5487 |
| | | RESULT 6 | |
| | | US-09-980-559A-9 | |
| | | ; Sequence 9, Application US/09980559A | |
| | | ; GENERAL INFORMATION: | |
| | | ; APPLICANT: Yanagi, Masayuki | |
| | | ; APPLICANT: Emerson, Suzanne | |
| | | ; APPLICANT: Buhk, Jens | |
| | | ; APPLICANT: Purcell, Robert | |
| | | ; TITLE OF INVENTION: CLONED GENOME OF INFECTIOUS HEPATITIS C | |
| | | ; TITLE OF INVENTION: VIRUSES OF GENOTYPE 2a AND USES THEREOF | |
| | | ; FILE REFERENCE: NIH255.00INP | |
| | | ; CURRENT FILING DATE: 2002-05-14 | |
| | | ; PRIOR APPLICATION NUMBER: PCT/US00/15446 | |
| | | ; PRIOR FILING DATE: 2000-06-02 | |
| | | ; PRIOR APPLICATION NUMBER: US 60/137,693 | |
| | | ; PRIOR FILING DATE: 1999-06-04 | |
| | | ; NUMBER OF SEQ ID NOS: 70 | |
| | | ; SOFTWARE: FastSeq for Windows Version 4.0 | |
| | | ; SEQ ID NO 9 | |
| | | ; LENGTH: 9611 | |
| | | ; TYPE: DNA | |
| | | ; ORGANISM: Hepatitis C virus | |
| | | US-09-980-559A-9 | |
| | | Query Match | |
| | | Best Local Similarity 91.1%; Pred. No. 0; | |
| | | Matches 1873; Conservative 0; Mismatches 183; Indels 0; Gaps 0; | |
| Qy | | 2 TGCGCGCTTATCACGGCTTATGCCACAGACAAAGAGCGCCCTTTGGATTGCATAATCAACA 61 | |
| Db | 3430 | TGGGGCCCATCAGCGGCGTAAGCCACAGACAGAAGGCGCTTGAGGTATTAATCAACA 3489 | |
| Qy | 62 | GCTTGACCGGCGGGACAAAACAGGTGAGGGTGAGGTTCAAGTGTGCAACTGCTG 121 | |
| Db | 3490 | GCCGTGACTGGCGGGACAAAACCAGGTGAGGGTGAGGTCAGATCGTGCAACTGCTA 3549 | |
| Qy | 122 | CCCAGACTTCTTGGAACCGTGATTAACGGGGGTGTGTGGACGTGTACCATGAGAGCG 181 | |
| Db | 3550 | CCCAAACCTTCTGTGCAACGTCATCAATGAGGATGTGAGCTGTCAACGGAGCGCG 3609 | |
| Qy | 182 | GAACAAGAACCATTTGCGTCACTTAAGGGTCTGTATTCAGATGTAGACCAATGTGACC 241 | |
| Db | 3610 | GAAAGAGGACCATGTGCATCAACCCAAGGTCCTGTCAATCAGATGTATACCAATGTGACC 3669 | |
| Qy | 242 | AAGACTCTGTAGGCTGTGGCGCGCTCCCAAGGTGCCCGCTCATTAACACATGACTTGGC 301 | |
| Db | 3670 | AAGACTTGTGTGGCTGTGGCGCGCTCTCTCAAGGTTCCCGCTCATTAACACCTGTACTGGC 3729 | |
| Qy | 302 | GCTCCTTGGAACCTTACTGTGTCAACGAGGACCGCGCATATCTCTGTGGCGCGAGCGG 361 | |
| Db | 3730 | GCTCCTTGGAACCTTACTGTGTCAACGAGGACCGCGCATATCTCTGTGGCGCGAGCGG 3789 | |
| Qy | 362 | GTGATGCGAGGGGAGAGCTGTCTTGCGCCCGGCTTATCTTTACTTGAAGAGCTCTCGG 421 | |
| Db | 3790 | GTGATGAGGGGGAGAGCTGTCTTGCGCCCGGCTTATCTTTACTTGAAGAGCTCTCTCGG 3849 | |
| Qy | 422 | GAGGCGCTTGTGTGCCCCGCGAGAGACATGCGGTAGGACATTTCAAGACCGCGGTATGCA 481 | |
| Db | 3850 | GAGGCGCTTGTGTGCCCCGCGAGAGACATGCGGTAGGACATTTCAAGAGCGCGGTATGCA 3909 | |
| Qy | 482 | CCCGTGTGAGTGGCTTAAGCGCGGTGTGACCTTCAATCCCGGTAGAGAGCTTGAAGCAACATGA 541 | |
| Db | 3910 | CCCGTGTGAGTGGCTTAAGCGCGGTGTGACCTTCAATCCCGGTAGAGAGCTTGAAGCAACATGA 3969 | |
| Qy | 542 | GGTCCCGCGGTGTTTCAAGACAACTCTTCCCGACAGAGATGCCCCAGAGCTTACCAAGTGG 601 | |
| Db | 3970 | GATCCCGCGGTGTTTCAAGAGCAACTCTTCCCGACAGAGATGCCCCAGAGCTTCAAGTGG 4029 | |
| Qy | 602 | CCCACTTGATGTCTCCACCGGCAAGCGGTAAAGACACCAAGTCCCGGCGCATATCGAG 661 | |

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Db 4030 CCCACCTGATGCTCCACCGGAGGCGTAAGAGCAACAAGATCCGGCTGGGTAGCGAG 4089
Qy 662 CTCAGGGCTACAAAGGTGCTGTCTCAACCCCTCCGTGTCTGAACAATAGGCTTTGGTG 721
Db 4090 CCCAGGGCTACAAAGGTGCTGTCTCAACCCCTCCGTGTCTGAACAAGGTGCTTTGGTG 4149
Qy 722 CTACATGTCGAAGGCGCATGGGATTGATCTTAACATAGAGATGGGGTGAAGACAATTA 781
Db 4150 CTACATGTCGAAGGCGCATGGGATTGATCTTAACATAGAGATGGGGTGAAGACAATTA 4209
Qy 782 CTACATGTCGAAGGCGCATGGGATTGATCTTAACATAGAGATGGGGTGAAGACAATTA 841
Db 4210 CCACCTGGAGCCCATCAGCTACGCTACCGCAAGTTCCTTGGCGAGCGGGGTGCT 4269
Qy 842 CAGGGGGTCTTATGACATTAATTTTGAAGAGTCCATCTCAAGATGCAACATCCA 901
Db 4270 CAGGAGGTCTTATGACATTAATTTTGAAGAGTCCATCTCAAGATGCAACATCCA 4329
Qy 902 TCTTGGGCAATTGGCACTGTCTTGAACGAAGAGACGGGGGGGCGAGACTGACTGTGC 961
Db 4330 TCTTGGGCAATTGGCACTGTCTTGAACGAAGAGACTGCGGGGGCGAGACTGTGTGC 4389
Qy 962 TCGCCACCGCTACCCCTCGGGCTCGGTCACTGTGCCCATCTTAACATCGAGAGTTC 1021
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Qy 1022 CTCTGTCCATACCGGAGAGATCCCTTTTATGGCAAGGCTATCCCTTTGAAGCAATTA 1081
Db 4450 CTCTGTCCATACCGGAGAGATCCCTTTTATGGCAAGGCTATCCCTTTGAAGTATCA 4509
Qy 1082 AGGGGGGAGACATCTCATCTTGTGCACTCAAGAGAGAGTGCAGAGCTGCAGCA 1141
Db 4510 AGGGGGGAGACATCTCATCTTGTGCACTCAAGAGAGAGTGCAGAGCTGCAGCA 4569
Qy 1142 AACTGTGCGGTGGGCGTCAATGCGGTGGCTTACTACCGCGGCTTGAATGTGTCCGTCA 1201
Db 4570 AGTGTGCGGTGGGCGTCAATGCGGTGGCTTACTACCGCGGCTTGAATGTGTCTGTC 4629
Qy 1202 TCCCGACAGTGTGACGTTGTGTGTGTGCAACTGACCGCTCATGACCGGCTTTACCG 1261
Db 4630 TCCCGACAGTGTGACGTTGTGTGTGTGCAACTGACCGCTCATGACCGGCTTTACCG 4689
Qy 1262 GGCACCTCGATGGGATGATGATGCAACGAGTGTGACCCGAGAGTGCAGCTTGACGC 1321
Db 4690 GGCACCTCGATGGGATGATGATGCAACGAGTGTGACCTGACAGAGTGCAGCTTGACGC 4749
Qy 1322 TTGACCCCTACCTTACCATTTGAGACATCAAGCTTCCCGAGAGTGTCTCCGTAATC 1381
Db 4750 TTGACCCCTACCTTACCATTTGAGACATCAAGCTTCCCGAGAGTGTCTCCGTAATC 4809
Qy 1382 AACGTGGGGTGAAGACTGGCAGAGGAGAGGCAAGGCACTTAACAGATTTTGGCACCGGG 1441
Db 4810 AACGTGGGGTGAAGACTGGCAGAGGAGAGGCAAGGCACTTAATGATTTTGGCACCGGG 4869
Qy 1442 AGGCTCTTCTGGCATGTTGACTCGTGTCTCTGCGAGTGTCTTGAACGGGGTGTG 1501
Db 4870 AGGCTCTTCTGGCATGTTGACTCGTGTCTCTGCGAGTGTCTTGAACGGGGTGTG 4929
Qy 1502 CTGTGATGAGCTTACGCGCGCGAGACCAAGTATGAGCTACGAGATACATGACACCC 1561
Db 4930 CTGTGATGAGCTTACGCGCGCGAGACCAAGTATGAGCTACGAGATACATGACACCC 4989
Qy 1562 CCGGACTTCCCGGTGTGCAAGACCATTTGGAATTTTGGAGGGGCTTTTACCGGCTCA 1621
Db 4990 CCGGACTTCCCGGTGTGCAAGACCATTTGGAATTTTGGAGGGGCTTTTACCGGCTCA 5049
Qy 1622 CCACATGAGCGGCACTTCTTCCAGACCAAGAGAGTGGGGAAAACCTTCCCTATC 1681
Db 5050 CTCTATGAGTGCACCTTTTATCCAGACCAAGAGAGTGGGGAAAACCTTCTTAC 5109
Qy 1682 TGTAGCTGACCAAGCACCGTGTGCTTGAAGCTCAAGCCCTCCCGTCTGTGGAGCC 1741
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Db 5110 TGTAGCTGACCAAGCACCGGCTGTGCTAGGGCTCAAGCCCTCCCGCATGTGGAGCC 5169
Qy 1742 AGATGGAAGGCTTGAATCCGTCTCAAGCCCATCTCATAGGGCAACACTTGTCTAT 1801
Db 5170 AGATGGAAGGCTTGAATCCGTCTCAAGCCCATCTCATAGGGCAACACTTGTCTAT 5229
Qy 1802 ATGACTGGGCGCTGTCCAGATGAGATGATCACCCTGACGCAACCACTGACCAAGTATCA 1861
Db 5230 ACAGACTGGGCGCTTTCAGATGAGATGATCACCCTGACGCAACCACTGACCAAGTATCA 5289
Qy 1862 TGACATGATATGTGCGCTGACTGAGAGTGTGTGACAGATACCTGGTGTCTGTGGCGGCG 1921
Db 5290 TGACATGATATGTGCGCTGACTGAGAGTGTGTGACAGATACCTGGTGTCTGTGGCGGCG 5349
Qy 1922 TTTGCTGCTTTTGGCGCGGATTTGCTTATCCAGGCGGTGTGATGAGTGAAGA 1981
Db 5350 TCTGCTGCTTGTGGCGCGGATTTGCTTATCCAGGCGGTGTGATGAGTGAAGA 5409
Qy 1982 TTTGCTGCTTGTGGCGCGGATTTGCTTATCCAGGCGGTGTGATGAGTGAAGA 2041
Db 5410 TGTCTTGTGCGGGAAGCGGCAATTATCTGACAGGAGGTTCTTACAGAGTTCG 5469
Qy 2042 ATGAATGGAAGTGTCT 2059
Db 5470 ATGAATGGAAGTGTCT 5487

RESULT 7
US-09-980-559B-3
; Sequence 3, Application US/09980559B
; GENERAL INFORMATION:
; APPLICANT: Yanagi, Masayuki
; APPLICANT: Emerson, Suzanne
; APPLICANT: Burk, Jens
; APPLICANT: Purcell, Robert
; TITLE OF INVENTION: CLONED GENOME OF INFECTIOUS HEPATITIS C
; FILE REFERENCE: NIH255.001NP
; CURRENT APPLICATION NUMBER: US/09/980,559B
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: PCT/US00/15446
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: US 60/137,693
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 9611
; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-09-980-559B-3

Query Match 85.6%; Score 1765.2; DB 5; Length 9611;
Best Local Similarity 91.1%; Pred. No. 0;
Matches 1875; Conservative 0; Mismatches 183; Indels 0; Gaps 0;

Qy 2 TGGCCCTATACCGGCTATGCTCCGAGACGAAGGGGCTTTTGGAGTCAATATACCA 61
Db 3430 TGGCCCTATACCGGCTATGCTCCGAGACGAAGGGCTTCTAGGGTATATATACCA 3489
Qy 62 GCTTACCGGCGGGGACAAAACAGGTGAGAGGTGAGATTGAGATCTGTCAACTGTCTG 121
Db 3490 GCTTACCGGCGGGGACAAAACAGGTGAGAGGTGAGATTGAGATCTGTCAACTGTCTG 3549
Qy 122 CCCAAGCTTCTTGGCAACTGATTTAACGGGGTGTGTGACTGTCTTACATGAGCCG 181
Db 3550 CCCAAGCTTCTTGGCAACTGATTTAACGGGGTGTGTGACTGTCTTACATGAGCCG 3609
Qy 182 GAAAGAGACATTTGCGTCACTTAAGGGTCTGTTATCCAGTATGATACCAATGAGACC 241
Db 3610 GAAAGAGACATTTGCGTCACTTAAGGGTCTGTTATCCAGTATGATACCAATGAGACC 3669
Qy 242 AAGACTGTAGGCTGGCCGCTCCCAAGGTGCCGCTCATTTAACACCATGACATTGGC 301
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Db 3670 AAGACTGTGGGGCTGGCCCGCTCCCAAGGTTCCCGCTCATTTGACACCCGTATCTGG 3729
Qy 302 GCTCTCGGACCTTTAACTGTGTACAGAGGACCGCGATGTCTTCTGTGGCCGACCGG 361
Db 3730 GCTCTCGGACCTTTAACTGTGTACAGAGGACCGCGATGTCTTCTGTGGCCGACCGG 3789
Qy 362 GTGATGGAGGGGGAGCGCTTTGGCCCGGCTATCTTACTTTGAAAGGCTCTGG 421
Db 3790 GTGATGGAGGGGGAGCGCTTTGGCCCGGCTATCTTACTTTGAAAGGCTCTGG 3849
Qy 422 GAGGCGCTCTGTGTGGCCCGGACGATGCGGTAGGCAATTTAGAGCGCGGTATGCA 481
Db 3860 GGGGTCGGGTGTGTGGCCCGGACGCGGTGGGCTATTTAGAGGCGCGGTGTGA 3909
Qy 482 CCCGTGAGTGGCTAAAGCGGTGGAATTTATCTGTGGAGAACTTAGGAGCAACATGA 3969
Db 3910 CCCGTGAGTGGCTAAAGCGGTGGAATTTATCTGTGGAGAACTTAGGAGCAACATGA 3969
Qy 542 GGTCCCGGTGTCTCAGACATCTCTCCGACAGAGTGCCGAGCTACCAAGTGG 601
Db 3970 GATCCCGGTGTCTCAGACATCTCTCTCAGAGAGTGCCGAGCTTCCAGGTGG 4029
Qy 602 CCCACTGATGCTCCACCGGACGGGTAGAGACCAAGGTCGCGCGCATACGAG 661
Db 4030 CCCACTGATGCTCCACCGGACGGGTAGAGACCAAGGTCGCGCGCATACGAG 4089
Qy 662 CTCAGGGCTCAAGGTCTGTGTCAACCCCTCGGTGTGCAACAATGGGCTTGTG 721
Db 4090 CCCAGGGCTCAAGGTGTGTGTCTCAACCCCTGTGTGTCAACGCTGGGCTTGTG 4149
Qy 722 CTATATGTCCAAAGGCCCATTTGGATTGATTCCTTAATCAAGGACTGGGGTGAAGCAATTA 781
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Qy 782 CTACTGGAGCCGACATCAAGTATTCACCTACGCAAGTCTTTCGCGAGCGGGGTGT 841
Db 4210 CCACGTGGAGCCGACATCAAGTATTCACCTACGCAAGTCTTTCGCGAGCGGGGTGT 4269
Qy 842 CAGGGGGTCTTATGACATTAATTTGTGACGAGTCCATCTCACGAGTGCACATCCA 901
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Qy 962 TGGCCACGCTACCCCTCCGGGCTCGTCACTGTGCCCATCTTAACATCGAGAGTGG 1021
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Qy 1082 AGGGGGGAGAAATCTCATCTTCTGCACTCAAAAGAAAGTGCACGAGCTCCGCGCA 1141
Db 4510 AGGGGGGAGAAATCTCATCTTCTGCACTCAAAAGAAAGTGCACGAGCTCCGCGCA 4569
Qy 1142 AACTGGTGGCTTTGGGCGTCAATGCGGTGGCTTACTACCGGAGCTTGTGTGCTGCA 1201
Db 4570 AGCTGTGGCAATTTGGGCAATGCGGTGGCTTACTACCGGAGCTTGTGTGCTGCA 4629
Qy 1202 TCCGACCAAGTGTGACGTTGTGTGTGGCAATGACGCGCTCATGACGCGGCTTTACG 1261
Db 4630 TCCGACCAAGTGTGACGTTGTGTGTGGCAATGACGCGCTCATGACGCGGCTTTACG 4689
Qy 1262 GGGACTTGCATTGCGGTAGATGAGTGAACAAGTGTGTACCCAGACATGCTTCAAGC 1321
Db 4690 GGGACTTGCATTGCGGTAGATGAGTGAACAAGTGTGTCTAGACAGTGTCTTCAAGC 4749
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Db 4810 AACGTCGGGGTATGAGCTGGCAGAGGGAAGCCAGGCACTTAATGATTTGGACCGGGGG 4869
Qy 1442 AGCGTCTTCTGTGAGCTGTGTGATCTGTGTCTTCTGTGAGAGTGTATGACGGGTTGTG 1501
Db 4870 AGCGGCTTCCGGGATGTTGATGATGCTGTGTGTCTGTGTGAGTGTATGACGGGCTGTG 4929
Qy 1502 CTGGTATGAGCTTACGCGCGCGAGACCAAGTATGAGCTTACAGACATTAACATCAACC 1561
Db 4930 CTGGTATGAGCTTACGCGCGCGAGACCAAGTATGAGCTTACAGACATTAACATCAACC 4989
Qy 1562 CGGACCTTCCGCTGTGCGCAAGACATCTTAATTTGGGAGGGGCTTTTACGGGTCTCA 1621
Db 4990 CGGACCTTCCGCTGTGCGCAAGACCAAGTATGAGCTTACAGACATTAACATCAACC 5049
Qy 1622 CCCACATGAGAGCCCACTTCTTATCCAGACAAAGCAAGTGGGAAAACTTCCCTATC 1681
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Qy 1682 TGTAGCGTACCAAGCCACGCTGTGCTTGAAGCTCAAGCCCTCCCGCTGTGGAGC 1741
Db 5110 TGTAGCGTACCAAGCCACGCTGTGCTTGAAGCTCAAGCCCTCCCGCTGTGGAGC 5169
Qy 1742 AGATGTGAAGTGTCTTGAATTCGCTCTCAGCCCACTTCAAGGGGCAACCTCTGTAT 1801
Db 5170 AGATGTGAAGTGTGTGATTCGCTTGAACCACTTCAAGGGGCAACCTCTGTAT 5229
Qy 1802 ATGAGCTGGGCGCTTCCAGATGAGTCAACCTTGAACCACTTCAAGGGGCAACCTCTGTAT 1861
Db 5230 ACAGACTGGGCGCTTCCAGATGAGTCAACCTTGAACCACTTCAAGGGGCAACCTCTGTAT 5289
Qy 1862 TGACATGATGTGTGCTGCTGAGTGTGTCACGATTAAGTGTGTCTGTGGCGGG 1921
Db 5290 TGACATGATGTGTGCTGCTGAGTGTGTCACGATTAAGTGTGTCTGTGGCGGG 5349
Qy 1922 TTCTGGCTGTGTGGCCCGCTTATGCTTATCAACAGGCTGTGTGTCTTATGAGTGA 1981
Db 5350 TCTGGCTGTGTGGCCCGCTTATGCTTATCAACAGGCTGTGTGTCTTATGAGTGA 5409
Qy 1982 TTCTGGCTGTGTGGCCCGCTTATGCTTATCAACAGGCTGTGTGTCTTATGAGTGA 2041
Db 5410 TGTCTTGTCCGGGAGCCGCGCAATTAACCTGACAGGAGGTTCTTACCAAGAGTTCG 5469
Qy 2042 ATGAATGGAAGTGTCT 2059
Db 5470 ATGAGATGGAAGTGTCT 5487

RESULT 8
US-09-980-559B-5
; Sequence 5, Application US/09980559B
; GENERAL INFORMATION:
; APPLICANT: Yanagi, Masayuki
; APPLICANT: Emerson, Suzanne
; APPLICANT: Burk, Jens
; APPLICANT: Purcell, Robert
; TITLE OF INVENTION: CLONED GENOME OF INFECTIOUS HEPATITIS C
; FILE REFERENCE: NIH25.001NP
; CURRENT APPLICATION NUMBER: US/09/980,559B
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: PCT/US00/15446
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: US 60/137,693
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 9611
; TYPE: DNA

RESULT 9
US-09-980-559B-7
; Sequence 7, Application US/09980559B
; GENERAL INFORMATION:
; APPLICANT: Yonagi, Masayuki
; APPLICANT: Emerson, Suzanne
; APPLICANT: Buhk, Jens
; APPLICANT: Purcell, Robert
; TITLE OF INVENTION: CLONED GENOME OF INFECTIOUS HEPATITIS C
; TITLE OF INVENTION: VIRUSES OF GENOTYPE 2a AND USES THEREOF
; FILE REFERENCE: NIH255.001NP
; CURRENT APPLICATION NUMBER: US/09/980,559B
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: PCT/US00/15446
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: US 60/137,693
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 7
; LENGTH: 9611
; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-09-980-559B-7

Query Match 85.6%; Score 1765.2; DB 5; Length 9611;
Best Local Similarity 91.1%; Pred. No. 0;
Matches 1875; Conservative 0; Mismatches 183; Indels 0; Gaps 0;

QY 2 TGGGCGCTATCAGCGGCTATGCGGAGACAAAGGGGCTTTGGAGTCAATATCACA 61
DB 3430 TGGGCGCTATCAGCGGCTATGCGGAGACAAAGGGGCTTTGGAGTCAATATCACA 3489
QY 62 GCTTACCGCGCGGAGCAAAAACAGGTGAGGTGAGGTGAGTCAATGCTGCTG 121
DB 3490 GCTTACCGCGCGGAGCAAAAACAGGTGAGGTGAGGTGAGTCAATGCTGCTG 3549
QY 122 CCCAGACTTTCTTGGAACCTGATTAACGGGGGTGTGTTGAGCTGTCAATGAGCCG 181
DB 3550 CCCAGACTTTCTTGGAACCTGATTAACGGGGGTGTGTTGAGCTGTCAATGAGCCG 3609
QY 132 GAACAAGACCTATGCGTCACTAAGGGTCTGTATCCAGATGTAACCAATGAGACC 241
DB 3610 GAACAAGACCTATGCGTCACTAAGGGTCTGTATCCAGATGTAACCAATGAGACC 3669
QY 242 AAGACCTGTAGAGTGGCGCGCTCCCAAGGTGCGGCTCATTAACACCATGACTTGG 301
DB 3670 AAGACCTGTAGAGTGGCGCGCTCCCAAGGTGCGGCTCATTAACACCATGACTTGG 3729
QY 302 GCTCTCTCGGACTTTTACCTGTACAGAGGACGCGGATGTCATTCCTGTGCGCGAG 361
DB 3730 GCTCTCTCGGACTTTTACCTGTACAGAGGACGCGGATGTCATTCCTGTGCGCGAG 3789
QY 352 GTGATGAGGAGGAGGAGGCTGTTTGGCGCGGCTATCTCTTAATTGAAAGGCTCTGG 421
DB 3790 GTGATGAGGAGGAGGAGGCTGTTTGGCGCGGCTATCTCTTAATTGAAAGGCTCTGG 3849
QY 422 GAGGCGCTGTGCTGAGCGCGGAGGACATGCGTGAAGCATATTCAAGGCGGGTATGA 481
DB 3850 GAGGCGCTGTGCTGAGCGCGGAGGACATGCGTGAAGCATATTCAAGGCGGGTATGA 3909
QY 482 CCCGTGAGTGGCTAAGCGGCTGAGCTTCACTCCCGTAGAGACTTGAAGAACCATGA 541
DB 3910 CCCGTGAGTGGCTAAGCGGCTGAGCTTCACTCCCGTAGAGACTTGAAGAACCATGA 3969
QY 542 GGTCCCGGCTGTTTCAAGCACTCTCCCAAGGAGTGGCGGAGGCTCAAGTGG 601
DB 3970 GGTCCCGGCTGTTTCAAGCACTCTCTCCCAAGGAGTGGCGGAGGCTCAAGTGG 4029
QY 602 CCCACTGTATCTCCCAAGGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 661

DB 4030 CCCACTGTATCTCCCAAGGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4089
QY 662 CTGAGGCGCTAAGAGTGTGAGTCAACCCCTCGTGTGCTCAACAATGAGGCTTTGGG 721
DB 4090 CCCAGGCTCAAGAGTGTGAGTCAACCCCTCGTGTGCTCAACGCTGGGCTTTGGG 4149
QY 722 CTATCATGTCAGAGGCGGATGAGTTCCTTAACATGAGAGTGGGAGGAGCAATTA 781
DB 4150 CTATCATGTCAGAGGCGGATGAGTTCCTTAACATGAGAGTGGGAGGAGCAATTA 4209
QY 782 CTATGTCAGAGGCGGATGAGTTCCTTAACATGAGAGTTCCTTAACATGAGAGTTC 841
DB 4210 CTATGTCAGAGGCGGATGAGTTCCTTAACATGAGAGTTCCTTAACATGAGAGTTC 4269
QY 842 CAGGAGGCTGTTATGAGTTCCTTAACATGAGAGTTCCTTAACATGAGAGTTC 901
DB 4270 CAGGAGGCTGTTATGAGTTCCTTAACATGAGAGTTCCTTAACATGAGAGTTC 4329
QY 902 TCTTGGGATGAGGAGTTCCTTAACATGAGAGTTCCTTAACATGAGAGTTC 961
DB 4330 TCTTGGGATGAGGAGTTCCTTAACATGAGAGTTCCTTAACATGAGAGTTC 4389
QY 962 TCGGACCGCTAAGGCTTCGAGGCTTCGAGTTCCTTAACATGAGAGTTC 1021
DB 4390 TCGGACCGCTAAGGCTTCGAGGCTTCGAGTTCCTTAACATGAGAGTTC 4449
QY 1022 CTCTGTCCATGAGGAGTTCCTTAACATGAGAGTTCCTTAACATGAGAGTTC 1081
DB 4450 CTCTGTCCATGAGGAGTTCCTTAACATGAGAGTTCCTTAACATGAGAGTTC 4509
QY 1082 AGGGGAGGAGGAGTTCCTTAACATGAGAGTTCCTTAACATGAGAGTTC 1141
DB 4510 AGGGGAGGAGGAGTTCCTTAACATGAGAGTTCCTTAACATGAGAGTTC 4569
QY 1142 AACTGTGCGGCTGAGGCTCAATGCGGCTTCATGAGGCTTCATGAGGCTTC 1201
DB 4570 AACTGTGCGGCTGAGGCTCAATGCGGCTTCATGAGGCTTCATGAGGCTTC 4629
QY 1202 TCCGACCAAGGAGTTCCTTAACATGAGAGTTCCTTAACATGAGAGTTC 1261
DB 4630 TCCGACCAAGGAGTTCCTTAACATGAGAGTTCCTTAACATGAGAGTTC 4689
QY 1262 GCGACTTGTGAGTTCCTTAACATGAGAGTTCCTTAACATGAGAGTTC 1321
DB 4690 GCGACTTGTGAGTTCCTTAACATGAGAGTTCCTTAACATGAGAGTTC 4749
QY 1322 TTGACCTTACCTTCAATGAGAGTTCCTTAACATGAGAGTTCCTTAAC 1381
DB 4750 TTGACCTTACCTTCAATGAGAGTTCCTTAACATGAGAGTTCCTTAAC 4809
QY 1382 AAGGTGAGGAGTTCCTTAACATGAGAGTTCCTTAACATGAGAGTTC 1441
DB 4810 AAGGTGAGGAGTTCCTTAACATGAGAGTTCCTTAACATGAGAGTTC 4869
QY 1442 AGGCTTGTGAGTTCCTTAACATGAGAGTTCCTTAACATGAGAGTTC 1501
DB 4870 AGGCTTGTGAGTTCCTTAACATGAGAGTTCCTTAACATGAGAGTTC 4929
QY 1502 CTGATGATGAGTTCCTTAACATGAGAGTTCCTTAACATGAGAGTTC 1561
DB 4930 CTGATGATGAGTTCCTTAACATGAGAGTTCCTTAACATGAGAGTTC 4989
QY 1562 CGGAGCTTCGAGTTCCTTAACATGAGAGTTCCTTAACATGAGAGTTC 1621
DB 4990 CGGAGCTTCGAGTTCCTTAACATGAGAGTTCCTTAACATGAGAGTTC 5049
QY 1622 CCCACATGAGGAGGCTTCCTTAACATGAGAGTTCCTTAACATGAGAGTTC 1681
DB 5050 CCCACATGAGGAGGCTTCCTTAACATGAGAGTTCCTTAACATGAGAGTTC 5109
QY 1682 TGTGAGGCTTACCAAGGAGTTCCTTAACATGAGAGTTCCTTAACATGAGAGTTC 1741
DB 5110 TGTGAGGCTTACCAAGGAGTTCCTTAACATGAGAGTTCCTTAACATGAGAGTTC 5169

| | | | |
|---|------|--|------|
| Oy | 1742 | IGAGTGTGGAAATGCTTGATTCGGCTCCAGACGCCACCCTCCAAAGGGCGCAACACTCTGCCTAT | 1801 |
| Db | 5170 | AGAATGTGAAGTTTGAATCCGCCCTTAACCACTCCTCAAAGGGCGCAACACCCCTGCCTAT | 5229 |
| Oy | 1802 | ATTAGACTGGGGCGCTGTCCAGATATGAAATGATCACCTGTGACCGCACCCAGTCAACCAATATATCA | 1861 |
| Db | 5230 | AACAAGCTGGGGCGCTGTCCAGATATGAAATGATCACCTGTGACCGCACCCAGTCAACCAATATATCA | 5289 |
| Oy | 1862 | TGACATGTATGTCCGCTGAACCTGAGGTCTGTACAGATGTAACCTGGGTGCTGTTGGCGGCG | 1921 |
| Db | 5290 | TGACATGATGTCCGCTGAACCTGAGGTCTGTACAGATGTAACCTGGGTGCTGTTGGCGGCG | 5349 |
| Oy | 1922 | TTCTGGCGCTTTTGGCGCGCGTATTTGCCATCCACAGCGCTGGGTGTCTAATAGGTATGA | 1981 |
| Db | 5350 | TCCTGGCTGTCTTGGCGCGCGTATTTGCCATCCACAGCGCTGGGTGTCTAATAGGTATGA | 5409 |
| Oy | 1982 | TTGTCTTGTCCGGAAAGCCGGCAATCATACCCGACAGGGAAGTCTCTACCGGGAGTTCC | 2041 |
| Db | 5410 | TCGTCTTGTCCGGAAAGCCGGCAATCATACCCGACAGGGAAGTCTCTACCGGGAGTTCC | 5469 |
| Oy | 2042 | ATTGAATGGAAAGTGTCT 2059 | |
| Db | 5470 | ATGAGATGAAAGAGTGTCT 5487 | |
| RESULT 10 US-09-980-559B-9 ; Sequence 9, Application US/09980559B ; GENERAL INFORMATION: ; APPLICANT: Yanagi, Masayuki ; APPLICANT: Emerson, Suzanne ; APPLICANT: Buhk, Jens ; APPLICANT: Purcell, Robert ; TITLE OF INVENTION: CLONED GENOME OF INFECTIOUS HEPATITIS C ; FILE REFERENCE: NIH255.00INP ; CURRENT APPLICATION NUMBER: US/09/980,559B ; CURRENT FILING DATE: 2002-05-14 ; PRIOR APPLICATION NUMBER: PCT/US00/15446 ; PRIOR FILING DATE: 2000-06-02 ; PRIOR APPLICATION NUMBER: US 60/137,693 ; PRIOR FILING DATE: 1999-06-04 ; NUMBER OF SEQ ID NOS: 70 ; SOFTWARE: FastSeq for Windows Version 4.0 ; SEQ ID NO 9 ; LENGTH: 9611 ; TYPE: DNA ; ORGANISM: Hepatitis C virus US-09-980-559B-9 | | | |
| Query Match 85.6%; Score 1765.2; DB 5; Length 9611; Best Local Similarity 91.1%; Pred. No. 0; Matches 1875; Conservative 0; Mismatches 183; Indels 0; Gaps 0; | | | |
| Oy | 2 | TGGCCCTCATCA CGGCTCATGCCCCAGACAGACAAAGGGGCTTTTGGATGATTAATCAACA | 61 |
| Db | 3430 | TGGGCCCATCA CGGCTCATAGCCCAGACAGACAGAGGGCTCTCTAGGGTGTATAATCAACA | 3489 |
| Oy | 62 | GCTTGACCGCGCGGACAAAAACAGGTGAGGGGTGAGGTTCAATGCTGTCAACTGCTG | 121 |
| Db | 3490 | GCCTGACTGGCGCGGACAAAAACAAAGTGAGGGGTGAGGTCCAGATGCTGTCAACTGCTG | 3549 |
| Oy | 122 | CCCGAGCTTTCTTGGCAACCTGCATTACGGGGGTGTGTTGACATGCTATCAACATGAGACG | 181 |
| Db | 3550 | CCCAAACTTCTCTGGCAACCTGCATCAATGGGGTATGCTGACATGTCTAACACAGGGGCG | 3609 |
| Oy | 182 | GAACAAGAGCACTTGTCTGCTCACTTAAGAGTCTCTGTATCCAATGTATCAACAATGTGAC | 241 |
| Db | 3610 | GAACAAGAGCACTTGTGCTATCAACCAAGGCTCTGTATCCAATGTATCAACAATGTGAC | 3665 |
| Oy | 242 | AAAGCTGTAGGCTGGCCCGCTCCCAAGGTGCCCGCTCAATTAACCATGACTTGGC | 301 |

| | | | | |
|---|---|------|--|------|
| D | b | 3670 | AAGACCTTGTGGGTGGCCCGCTCTCTCAAGGTTCGCGCTCATTTGACACCTGTACTGG | 3729 |
| O | y | 302 | GCTCTCTGGACCTTTACCTGTGTCAAGAGCAACGCCAGTGTCACTCTGTGGCCGACGG | 361 |
| D | b | 3730 | GCTCTCTGGACCTTTACCTGTGTCAAGAGCAACGCCAGTGTCACTCTCTGTGGCCGACGG | 3789 |
| O | y | 362 | GTGATGGCAGGGGAGGCTGTTTCGGCCCGGCTATCTCTTACTTGAAGAGCTCTCGG | 421 |
| D | b | 3790 | GTGATTCACAGGGGATGAGCTCTCTTTCGGCCCGGCTCTCTTACTTGAAGAGCTCTCGG | 3849 |
| O | y | 422 | GAGGACCTCTGTGTGCCCCGACAGACATCCCGTAGGCAATTCAGAGCCGCGTATGCA | 481 |
| D | b | 3850 | GGGGTCCGCTGTGTGTGCCCCGACAGACACGCCGTGGGCTATTCAGGGCCGCGGTGTGCA | 3909 |
| O | y | 482 | CCCGTGAAGTGTGAAGCGGTGACTTCACTCCCGTAGAGAGCTTGAAGCAACATGA | 541 |
| D | b | 3910 | CCCGTGAAGTGTGAAGCGGTGACTTCACTCTGTGAGAGACTTAGGAGCAACATGA | 3969 |
| O | y | 542 | GGTCCCCGGGTGTTTCAAGACAACTCTCTCCCAACAGAGTGGCCCAAGCTACCAATGG | 601 |
| D | b | 3970 | GATCCCCGGGTGTTTCAAGACAACTCTCTCAACAGAGTGGCCCAAGCTTCCAGTGG | 4029 |
| O | y | 602 | CCCACTGCAATGCTCCCAACGGGACAGGGTGAAGACCAAGGTCCCGACGATACGACG | 661 |
| D | b | 4030 | CCCACTGCAATGCTCCCAACGGGACAGGGTGAAGACCAAGGTCCCGCTGTGTACGACG | 4089 |
| O | y | 662 | CTCAGGGCTACAAAGTGTGGTGTCAACCCCTCTCGTGTGCAACAATGGGCTTTGGT | 721 |
| D | b | 4090 | CCCAAGGCTACAAAGTGTGGTGTCAACCCCTCTGTGTGTGCAACGCTGGGCTTTGGT | 4149 |
| O | y | 722 | CTTACATGTCCAAAGGCCCATGGGATTTGATCTCTAACATCAGAGCTGGGGGTGAGCAATTA | 781 |
| D | b | 4150 | CTTACATGTCCAAAGGCCCATGGGGTTGATCTCTAATACAGACCGGGGTGAGCAATTA | 4209 |
| O | y | 782 | CTACTGGCAGGCCGATACAGTAATCCACTACGGCAGATTCTCTTGCGGACGGCGGGAGTT | 841 |
| D | b | 4210 | CCACTGGAGGCCCATACAGTAATCCACTACGGCAGATTCTCTTGCGGACGGCGGGAGTT | 4269 |
| O | y | 842 | CAGGGGATGCTTATGACATATATTTGTGACGAGTGCACACTCCACGGATGCAACATCA | 901 |
| D | b | 4270 | CAGGAGGATGCTTATGACATATATTTGTGACGAGTGCACACTCCACGGATGCAACATCA | 4329 |
| O | y | 902 | TCTTGGGCAATTGGACATGTCTCTTGAACCAAGCAGAGCCGGGGGGCGAGACTGACTGTGC | 961 |
| D | b | 4330 | TCTTGGGCAATCGGACATGTCTCTTGAACCAAGCAGAGCTGGGGGGCGAGACTGTGTGC | 4389 |
| O | y | 962 | TGCGCACCGGCAACCCCTCCGGGGCTCGGTCACTGGCCCATCTCTAATCGAGGAGGTTG | 1021 |
| D | b | 4390 | TGCGCACCTGTACCCCTCTCCGGGCTCGGTCACTGTGTCCATCTTACATGAGGAGGTTG | 4449 |
| O | y | 1022 | CTCTGTCCACTTACCGGAGAGTCCCTTTTATGCGAAGGCTATTCCTCTTGAAACAATTA | 1081 |
| D | b | 4450 | CTCTGTCCACCAACCGGAGAGTCCCTTTTACGCGAAGGCTATCCCTCTGAGGTATCA | 4509 |
| O | y | 1082 | AGGGGGGAGACATCTCATCTTTCTGCACTTCAAGAAAGTAGTGACAGTGTGCGCGCA | 1141 |
| D | b | 4510 | AGGGGGGAGACATCTCATCTTTCTGCACTTCAAGAAAGTAGTGACAGTGTGCGCGCA | 4569 |
| O | y | 1142 | AACGTGTGCGTTGGGGGTCAATGCGGTGGCTTACTACGGGGCTTGAAGTGTGCGTCA | 1201 |
| D | b | 4570 | AGCTGTGTGCAATGGGGCATCAATGCGGTGGCTTACTACCGGGGCTTGAAGTGTGCGTCA | 4629 |
| O | y | 1202 | TCCCGACCAAGTGTGACGTTGTGCTGTGGCAACTGACGGCTCTATGACGGGCTTTACG | 1261 |
| D | b | 4630 | TCCCGACCAAGGGGGAGTGTGTGCTGTGTGACCGAATGCTCTATGACTGTGCTTTACG | 4689 |
| O | y | 1262 | GCGACTTCGATTGGGTGATGACTGCAACAGTGTGTACCCACAGACAGTGTGACTTCAGCC | 1321 |
| D | b | 4690 | GCGACTTCGACTGTGATGACTGCAACAGTGTGTCACTCAGACAGTGTGACTTCAGCC | 4749 |
| O | y | 1322 | TTGACCTTACTTACCATTTGAGACATCAACGTTTCCCAAGAGTGTGTCTCCCGGTACTC | 1381 |
| D | b | 4750 | TTGACCTTACTTATCATTTGAGACCAACAGCTCTCCCAAGAGTGTGTCTCCAGAGACTC | 4809 |


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OY 1382 AACGTGGGGGTAGAGACTGGCAGAGGGAGGCCAGGCACTACAGATTGTGGCACC GGGG 1441
DB 4810 AACGCCGGGGCAGACACTGGCAGGGGGAAAGCCAGGCACTATAGATTGTGGCACC GGGG 4869
OY 1442 AGCGTCCTTTCTGGCATGTTTGAACCTGTCGTCTCTCGGAGTGCTATGACCGGGTTGTG 1501
DB 4870 AAGCGCCCTCCGGCATATTTGCACTGTCCTGCTCTCTGAGATGCTATGACCGGGCTGTG 4929
OY 1502 CTTGGTATGAGCTTACCGCCCGCGAGAACACAGTTAGGCTTACGAGCATACATGAACCC 1561
DB 4930 CTTGGTATGAGCTACAGCCCGCGAGACTACAGTTAGGCTACGAGCGTACATGAACACC 4989
OY 1562 CGGGAATTCGCCGTGTGCAGAGCACTTGAATTTTGGAGGGGCTCTTTACGGGTCTCA 1621
DB 4990 CGGGGCTTCCCGTGTGCAGAGCACTTGAATTTTGGAGGGGCTCTTTACGGGGCTCA 5049
OY 1622 CCCACATAGACGCCCACTTCTCTATCCGACAAAGCAGAGTGGGGAAAACTTCCCTATC 1681
DB 5050 CTCATATAGATGGCCACTTTTATCCAGACAAAGCAGAGTGGGGAAACTTCTTACC 5109
OY 1682 TGGTACGCTACCAAGCCACCGTGTGCGCTAGAGCTCAAGCCCTTCCCGTGTGGAGC 1741
DB 5110 TGGTACGCTACCAAGCCACCGTGTGCGCTAGAGCTCAAGCCCTTCCCGTGTGGAGC 5169
OY 1742 AAGTGGGAAGTGTCTGATCCGTCTCAAGCCACCTCCATAGGGGCCAACACTCTGTAT 1801
DB 5170 AAGTGGGAAGTGTGTGATCCGTCTCAAGCCACCTCCATAGGGGCCAACACTCTGTAT 5229
OY 1802 ATAGACTGGGCGCGTCTCAGAAATGAAGTCACTCTGACGACACCCAGTCAAGATATATCA 1861
DB 5230 ACAGACTGGGCGCGTGTTCAGAAATGAAGTCACTCTGACGACACCCAGTCAAGATATATCA 5289
OY 1862 TGACATGATATGTGCGCTGACCTGAGAGTCTGTCAAGAGTACTGTGGTGTGGCGG 1921
DB 5290 TGACATGATATGTGCGCGGACCTGAGAGTCTGTCAAGAGTACTGTGGTGTGGCGG 5349
OY 1922 TTCTGCTCTCTTGGCGCGCTATTTGCTATCCAGAGCTGTGTGTGCTATATAGTAGA 1981
DB 5350 TTCTGCTCTCTTGGCGCGCGCTATTTGCTGTCAAGAGCTGTGTGTGCTATATAGTAGA 5409
OY 1982 TTGCTTTGTCGGGAAAGCCGGCAATCATCCCGACAGGAAAGTCTCTACCGGGAGTTG 2041
DB 5410 TCGCTTGTTCGGGAAAGCCGGCAATTACTGACAGGAGTTCTCTACAGAGTTG 5469
OY 2042 ATGAATGGAAGAGTCT 2059
DB 5470 ATGAGATGGAAGAGTCT 5487

RESULT 11
US-60-752-866-8
/ Sequence 8, Application US/60752866
/ GENERAL INFORMATION:
/ APPLICANT: Roche Palo Alto LLC
/ APPLICANT: Dietrich, Paul
/ APPLICANT: Le Pogam, Sophie
/ APPLICANT: Kosaka, Alan
/ TITLE OF INVENTION: HCV Shuttle Replicon Vectors
/ FILE REFERENCE: R0277A-PRO
/ CURRENT APPLICATION NUMBER: US/60/752,866
/ CURRENT FILING DATE: 2005-12-21
/ NUMBER OF SEQ ID NOS: 33
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 8
/ LENGTH: 10644
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Nucleotide sequence of plasmid pBS-1_1a_5'AsiSI_1acZamC_3'ResIII
US-60-752-866-8

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|-----------------------|--------------|---------------|-----------------|---------------|
| Query Match | 83.8% | Score 1727.8; | DB 12; | Length 10644; |
| Best Local Similarity | 89.9%; | Pred. No. 0; | | |
| Matches 1852; | Conservative | 0; | Mismatches 207; | Indels 0; |
| | | | | Gaps 0; |

| | | | |
|----|------|--|------|
| OY | 1 | ATGGGGCTATACAGGCGCTATGCCAGAGACAAAGGGGCGCTTTGGATGCAATATACAC | 60 |
| Db | 3347 | ATGGGGCTATATAGGCGCTACTCTCCACACAGCGGAGCGTACTTGGCTGATCATCACT | 3406 |
| OY | 61 | AGCTTGAACCGGCGCGGACAAAAAACAGGTGAGGGGTGAGTTTCAGATCGTCAACTGCT | 120 |
| Db | 3407 | AGCTCAACAGGCGGGACAGGAACAGGTGAGGGGGAGGTCCAAAGTGTCTCACCGGCA | 3466 |
| OY | 121 | GCCCAGACTTTCTTTGGCACTTGATTAACGGGGTGTGTGGACTGTCTACATGAGCC | 180 |
| Db | 3467 | ACACAATCTTCTCTGGGCACTGTGTCMAATGGCTGTGTGGACGTCTATCATGATGGCC | 3526 |
| OY | 181 | GGAAACAAGGACATTTGGCGTCACTTAAGGGGTCTGTATTCGAGATGTACCAATAGTGAAC | 240 |
| Db | 3527 | GGCTCAAGACCTCTTGGCGGCGCCAAAGGGCCCAATATACCAATATGTACCAATATGTGAC | 3586 |
| OY | 241 | CAAGACTCTGTAAGCTGGCGCGCTCCCAAGGTGCCCGCTCATTTAACCAATGCACTTGC | 300 |
| Db | 3587 | CAAGACTCTTGGGCTGGCGCGCTCTCTCAAGAGTTCCGCTCATTGACACCTGTACTGCG | 3646 |
| OY | 301 | GGCTCTCTGGACCTTTTACCTGTGTACAGAGGACCGCGCATTTCTCTGTGTGGCCGACGG | 360 |
| Db | 3647 | GGCTCTCTGGACCTTTTACCTGTGTACAGAGGACCGCGCATTTCTCTGTGTGGCCGACGG | 3706 |
| OY | 361 | GGTATGAGCAGGGGACGCTGCTTTTGGCGCGCGCTTACTTCTTAAAGGCTCTGCG | 420 |
| Db | 3707 | GGTATGAGCAGGGGTAGCTGTCTTTGGCGCGCGCATTTCTTCTTAAAGGCTCTGCG | 3766 |
| OY | 421 | GGAGGCGCTCTGCTGTGCGCCCGGACAGACATGCGTGAAGCATTTCAAGCGCGGTATGC | 480 |
| Db | 3767 | GGGGGTCCGCTGTGTGTCCCGCGGGACACGCGCTGGGGCTTAATCAAGGGCGCGGTGTGC | 3826 |
| OY | 481 | ACCGGTGAAGTGGTTAAGCGGTGGAATTCATCCCGTGAAGACTTAAGACAAACATG | 540 |
| Db | 3827 | ACCGGTGAAGTGGCTTAAAGCGGTGGAATTTATCCCTGTGAGAACTAAGGACAAACATG | 3886 |
| OY | 541 | AGGTCTCCCGGTGTCTCAGACAACTCCTCCACACAGAGTGCCTCCAGAGCTAACAAAGT | 600 |
| Db | 3887 | AGATCTCCCGGTGTCTCAGACAACTCCTCTCCACACAGAGTGCCTCCAGAGTTCACAGT | 3946 |
| OY | 601 | GCCCACTGCATGCTCCACCGGACGGGTGAAGACCAAGGTCCCGCGCGATACGCA | 660 |
| Db | 3947 | GCCCACTGCATGCTCCACCGGACGGGTGAAGACCAAGGTCCCGCGCTGCCTACGCA | 4006 |
| OY | 661 | GCTAAGGCTTACAGAGTGTGTGTGCTCAACCCCTCGTGTGGAACAATAGGGCTTTGGT | 720 |
| Db | 4007 | GCCAGGGCTTACAGAGTGTGTGTGCTCAACCCCTCTGTGTGGAACGCTGGGCTTTGGT | 4066 |
| OY | 721 | GCTTACATGTCCAAAGGCGCATGGGATGTATCTTAATCAGACTGGGGTGAAGACAAT | 780 |
| Db | 4067 | GCTTACATGTCCAAAGGCGCATGGGGTGTATCTTAATCAGAGCGGGGTGAAGACAAT | 4126 |
| OY | 781 | ACTACTGGCAGCCCGGATCAAGTATTTCCACTCAGGCAAGTTCTTGTGCCACGGCGGGTGT | 840 |
| Db | 4127 | ACCACTGGCAGCCCGGATCAAGTATTTCCACTCAGGCAAGTTCTTGTGCCACGGCGGGTGC | 4186 |
| OY | 841 | TCAGGGGGGTCTTATGACATTAATTTGTGACAGATGSCACTCAGGATGCAACATCC | 900 |
| Db | 4187 | TCAGAGAGTGTATTATGACATTAATTTGTGACAGATGSCACTCAGGATGCCACATCC | 4246 |
| OY | 901 | ATCTTGGGCAATGGCACTGTCTTGAACAAGCAGAGACCGCGGGGGCGAAGCTGACTGTG | 960 |
| Db | 4247 | ATCTTGGGCAATCGGCACTGTCTTGAACAAGCAGAGACTCGGGGGCGAAGCTGTGTGTG | 4306 |
| OY | 961 | CTGGCACAACGCTACCCCTCGGGGTCTCGTACTGTGTGCCATCTTAATCATTCAGAGAGTT | 1020 |
| Db | 4307 | CTGGCACAACGCTACCCCTCGGGGTCTCGTACTGTGTGCCATCTTAATCATTCAGAGAGATT | 4366 |
| OY | 1021 | GCTCTGTCACTACCGAGAGATCCCTTTTATGGCAAGGCTATTCCTTGAAGCAATT | 1080 |

|||||
4367 GCTCTGTCCACCAACCGAGAGATCCCTTTTACGGCAAGGCTATCCCTCGAGGTGATTC 4426
|||
QY 1081 AAGGGGGGAGACATCTCATCTTTGCGCACTCAAGAGAGTGCAGAGCTCGCCGCA 1140
|||
Db 4427 AAGGGGGGAGACATCTCATCTTTGCGCACTCAAGAGAGTGCAGAGCTCGCCGCG 4486
|||
QY 1141 AATCGTGTGGGCGCTCAATGCGGCGTTTCTACCGGGCGCTTGAATGTGCGCTC 1200
|||
Db 4487 AAGCTGTGTGCAATGGGCAATGACCGGCTTACTACCGGCTTGAATGTGCGCTC 4546
|||
QY 1201 ATCCGACCAAGTGTGACGTTGTGTGTGTGCACTGACGCGCTGATGACCGCTTTTACC 1260
|||
Db 4547 ATCCGACCAAGGCGGATGTGTGTGTGTGTGCACTGACGCGCTGATGACGCTTTTACC 4606
|||
QY 1261 GCGGACTTGTGATTCGCTGATTAACCTGCAACAGTGTGTGCACTGACGCGCTTACAC 1320
|||
Db 4607 GCGGACTTGTGATTCGCTGATTAACCTGCAACAGTGTGTGCACTGACGCGCTTACAC 4666
|||
QY 1321 CTGTAACCTTACCTTACCAATGAGCAATCAAGCTTCCCGAGAGTGTGTGCTCCGCTACT 1380
|||
Db 4667 CTGTAACCTTACCTTACCAATGAGCAATCAAGCTTCCCGAGAGTGTGTGCTCCGCTACT 4726
|||
QY 1381 CAACGTCGCGGTGAGACTGTCAGAGGAGGAGCCAGGATCTACAGATTTGTGCGACCGGCG 1440
|||
Db 4727 CAACGTCGCGGTGAGACTGTCAGAGGAGGAGCCAGGATCTACAGATTTGTGCGACCGGCG 4786
|||
QY 1441 GAGCGTCTTGTGCGCATGTTTGAATGCTGTGTGTGTGTGCGAGTGTGATGACCGGCTGT 1500
|||
Db 4787 GAGCGCGCTTGTGCGCATGTTTGAATGCTGTGTGTGTGTGCGAGTGTGATGACCGGCTGT 4846
|||
QY 1501 GCTTGGTATGAGCTTACGCGCGCGGAGACACAGTATGAGCTACGAGATACATGAACACC 1560
|||
Db 4847 GCTTGGTATGAGCTTACGCGCGCGGAGACACAGTATGAGCTACGAGATACATGAACACC 4906
|||
QY 1561 CCGGGACTTCCGCTGTGCCAAGACCATCTTGAATTTTGGAGGCGCTTTTACCGGCTTC 1620
|||
Db 4907 CCGGGGCTTCCGCTGTGCCAAGACCATCTTGAATTTTGGAGGCGCTTTTACCGGCGCTTC 4966
|||
QY 1621 ACCCATATGAGCGCCATCTTCTATTCAGACAAAGCAGAGTGGGAAAACCTTCCCTAT 1680
|||
Db 4967 ACTCATATGATGCGCCATCTTCTATTCAGACAAAGCAGAGTGGGAAAACCTTCCCTAT 5026
|||
QY 1681 CTGGATAGCTACCAAGCCACCGTGTGCTAGAGCTCAAGCCCTCCCGCTGCGGAGAC 1740
|||
Db 5027 CTGGATAGCTACCAAGCCACCGTGTGCTAGAGCTCAAGCCCTCCCGCTGCGGAGAC 5086
|||
QY 1741 CAGATGTGAGAGTCTTGAATCCGCTCAAGCCCACTTCATGTGGCCACACCTTGTCTA 1800
|||
Db 5087 CAGATGTGAGAGTCTTGAATCCGCTCAAGCCCACTTCATGTGGCCACACCTTGTCTA 5146
|||
QY 1801 TTTAGACTGGGCGCTGTCCAGAAATGAATGACCTTGAAGCAGCCAGTCAACAAATATATC 1860
|||
Db 5147 TTAGACTGGGCGCTGTGTCAAGATGAATGACCTTGAAGCAGCCAGTCAACAAATATATC 5206
|||
QY 1861 ATGACATGATATGCGGCTGACCTGAGAGGCTGACAGAGTACCTGGGTGTGCTGTGGCGGC 1920
|||
Db 5207 ATGACATGATATGCGGCTGACCTGAGAGGCTGACAGAGTACCTGGGTGTGCTGTGGCGGC 5266
|||
QY 1921 GTTCTGCTGCTTTGGCGCGATTTGCTCATCCACAGAGCTGCTGTCTATGATGATAG 1980
|||
Db 5267 GTTCTGCTGCTTTGGCGCGATTTGCTCATCCAGAGCTGCTGTCTATGATGATAG 5326
|||
QY 1981 ATTGTCTTGTCCGAAAAGCCGCAATCATACCGACAGGAAAGTCTCTTACCGGAGATTC 2040
|||
Db 5327 ATCTGTCTTGTCCGAAAAGCCGCAATCATCATGACAGGAGGATCTCTTACAGGAGATTC 5386
|||
QY 2041 GATGAATAAGAAAGATGCT 2059
|||
Db 5387 GATGATGAATAAGATGCT 5405

RESULT 12

US-60-752-866-2
; Sequence 2, Application US/60752866
; GENERAL INFORMATION:
; APPLICANT: Roche Palo Alto LLC
; APPLICANT: Dietrich, Paul
; APPLICANT: Le Pogam, Sophie
; APPLICANT: Kosaka, Alan
; APPLICANT: Najera, Isabel
; TITLE OF INVENTION: HCV Shuttle Replicon Vectors
; FILE REFERENCE: R0277A-PRO
; CURRENT APPLICATION NUMBER: US/60/752, 866
; CURRENT FILING DATE: 2005-12-21
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 2
; LENGTH: 11509
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Nucleotide sequence of plasmid pSS-1
US-60-752-866-2

Query Match 83.8%; Score 1727.8; DB 12; Length 11509;
Best Local Similarity 89.9%; Pred. No. 0;
Matches 1852; Conservative 0; Mismatches 207; Indels 0; Gaps 0;
QY 1 ATGGGCGCTATCAGCGCTATATGCGCAGAGCAAGGGGCGCTTTGGAGTGCATATCAC 60
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Db 3347 ATGGGCGCTATATCAGCGCTATATGCGCAGAGCAAGGGGCGCTTTGGAGTGCATATCAC 3406
|||
QY 61 AGCTTGACCGGCGCGGACAAACACAGGTGAGAGGTGAGTTGAGATGCTGTCACTGCT 120
|||
Db 3407 AGCTTGACCGGCGCGGACAGGAACAGGTGAGAGGTGAGTTGAGATGCTGTCACTGCT 3466
|||
QY 121 GCCCAGCTTTCTTGGCACTGCTATTAACGCGGTGTGTGAGCTGTCTACATGAGGCC 180
|||
Db 3467 ACACATCTTTCTTGGCACTGCTATTAACGCGGTGTGTGAGCTGTCTACATGAGGCC 3526
|||
QY 181 GGAACAAAGACATTTGCGCTACCTTAAAGGTGCTGTATTCAGATGTACCAATGTGAGC 240
|||
Db 3527 GGTCAAAAGACCTTTGCGCTACCTTAAAGGTGCTGTATTCAGATGTACCAATGTGAGC 3586
|||
QY 241 CAAGACTCTGATGAGCTGCGCTCCCGAAGGTGCGCTCATTTAAACCATGACCTTTC 300
|||
Db 3587 CAAGACTCTGATGAGCTGCGCTCCCGAAGGTGCGCTCATTTAAACCATGACCTTTC 3646
|||
QY 301 GGTCTCTGAGACTTTTACCTGTGTCAAGAGCAGCGGATGATCTCTGTGCGCGAGCG 360
|||
Db 3647 GGTCTCTGAGACTTTTACCTGTGTCAAGAGCAGCGGATGATCTCTGTGCGCGAGCG 3706
|||
QY 361 GGTGATGAGAGGGGAGCGCTGTTTGGCGCGGCTATCTTTTGAAGAGCTCTTCG 420
|||
Db 3707 GGTGATGAGAGGGGAGCGCTGTTTGGCGCGGCTATCTTTTGAAGAGCTCTTCG 3766
|||
QY 421 GGAGGCGCTTGTGCTGTGCGCGCAGAGCATGCGGTGAGCATATTCAGAGCGCGTATGC 480
|||
Db 3767 GGAGGCGCTTGTGCTGTGCGCGCAGAGCATGCGGTGAGCATATTCAGAGCGCGTATGC 3826
|||
QY 481 ACCCGTGAATGAGTGAAGCGGTGAGCTTCAATCCCGTGAAGAGCTTGAAGCAACCATG 540
|||
Db 3827 ACCCGTGAATGAGTGAAGCGGTGAGCTTCAATCCCGTGAAGAGCTTGAAGCAACCATG 3886
|||
QY 541 AGGTCCCGGCTGTCTGAGCAACCTCCACAGAGAGTCCCGAGAGCTACCAAGTG 600
|||
Db 3887 AGGTCCCGGCTGTCTGAGCAACCTCCACAGAGAGTCCCGAGAGCTACCAAGTG 3946
|||
QY 601 GCCCAGCTGATGCTCCCAACCGGCGAGCGGTGAAGACCAAGGTCCCGCGCATATGCA 660
|||
Db 3947 GCCCAGCTGATGCTCCCAACCGGCGAGCGGTGAAGACCAAGGTCCCGCGCATATGCA 4006
|||
QY 661 GCTCAGGCTACAGAGTGTGTCTCAACCTCTCGTTGTCTGCAACATGGGCTTTGGT 720
|||
Db 4007 GCCCAGGCTACAGAGTGTGTGTCTCAACCTCTGTGTGTCTGCAACAGCTGGGCTTTGGT 4066

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Qy 721 GCTTACATGTCMAAGGCCCATGGGATTTGATTCCTAATCAGAGACTGGGGTGAACAATT 780
Db 4067 GCTTACATGTCMAAGGCCCATGGGATTTGATTCCTAATCAGAGACTGGGGTGAACAATT 4126
Qy 781 ACTACTGGAGGCCGATTCAGATATTCACCTACGGCAAGTTCCTTGGCCGACGGCGGGTGT 840
Db 4127 ACCACTGGAGGCCCATTCAGATATTCACCTACGGCAAGTTCCTTGGCCGACGGCGGGTGT 4186
Qy 841 TCAGAGGGGTGCTTATATGATATTAATTTGTGAGAGATGCCACTCCACGATGGAATATCC 900
Db 4187 TCAGAGGGGTGCTTATATGATATTAATTTGTGAGAGATGCCACTCCACGATGGAATATCC 4246
Qy 901 ATCTTGGGATTTGGCACTGCTCTTGAACAAGAGAGACCGGGGGGCGAGACTGATGTG 960
Db 4247 ATCTTGGGATTTGGCACTGCTCTTGAACAAGAGAGATGCCGGGGGCGAGACTGATGTG 4306
Qy 961 CTGCGCACCGCTACCCCTCCGGGCTCGTCACTGTGCCCATCTTAACATCGAGAGATT 1020
Db 4307 CTGCGCACCGCTACCCCTCCGGGCTCGTCACTGTGCCCATCTTAACATCGAGAGATT 4366
Qy 1021 GCTCTGTCCACTACCGGAGAGATCCCTTTTATGGCAAGGCTATTCCTTGAAGCAATT 1080
Db 4367 GCTCTGTCCACTACCGGAGAGATCCCTTTTATGGCAAGGCTATTCCTTGAAGGATC 4426
Qy 1081 AAGGGGGGAGACATCTCATCTTCTGSCACTCAAAAGAGAGAGAGAGAGAGCTCGCCGA 1140
Db 4427 AAGGGGGGAGACATCTCATCTTCTGSCACTCAAAAGAGAGAGAGAGAGAGCTCGCCGA 4486
Qy 1141 AAATGCTGTCGCTTGGGCGTCAATGCGGCTTACTACCGCGGCTTGAATGTGCTGTC 1200
Db 4487 AAGCTGCTGTCGCTTGGGCGTCAATGCGGCTTACTACCGCGGCTTGAATGTGCTGTC 4546
Qy 1201 ATCCGACCAAGTGTGATGCTTGTGCTGTGGCACTGAGCGCTTACACCGGCTTTACC 1260
Db 4547 ATCCGACCAAGTGTGATGCTTGTGCTGTGGCACTGAGCTTACACCGGCTTTACC 4606
Qy 1261 GGGGACTTGATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320
Db 4607 GGGGACTTGATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4666
Qy 1321 CTGTAACCTTACCTTCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380
Db 4667 CTGTAACCTTACCTTCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4726
Qy 1381 CAACGTCGGGCTTGAAGCTGCGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
Db 4727 CAACGTCGGGCTTGAAGCTGCGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4786
Qy 1441 GAGCGCTCTTGGGCAATGTTTGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
Db 4787 GAGCGCTCTTGGGCAATGTTTGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4846
Qy 1501 GCTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
Db 4847 GCTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4906
Qy 1561 CCGGGAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620
Db 4907 CCGGGAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4966
Qy 1621 ACCCATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1680
Db 4967 ACCCATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5026
Qy 1681 CTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740
Db 5027 CTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5086
Qy 1741 CAGATGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1800
Db 5087 CAGATGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5146

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Qy 1801 TATAGACTGGGCGCTGTCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1860
Db 5147 TATAGACTGGGCGCTGTCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5206
Qy 1861 ATGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1920
Db 5207 ATGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5266
Qy 1921 GTTCTGGGCTGCTTGGGCGGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1980
Db 5267 GTTCTGGGCTGCTTGGGCGGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 5326
Qy 1981 ATTGCTTGTCCGAAAGCGGCAATCATACCGGACAGAGAGAGAGAGAGAGAGAGAGAGAG 2040
Db 5327 ATGCTGCTGTCCGAAAGCGGCAATCATACCGGAGAGAGAGAGAGAGAGAGAGAGAGAG 5386
Qy 2041 GATGAATGAAAGAGTCT 2059
Db 5387 GATGAATGAAAGAGTCT 5405

RESULT 13
US-60-752-866-7
; Sequence 7, Application US/60752866
; GENERAL INFORMATION:
; APPLICANT: Roche Palo Alto LLC
; APPLICANT: Dietrich, Paul
; APPLICANT: Le Pogam, Sophie
; APPLICANT: Kosaka, Alan
; APPLICANT: Najera, Isabel
; TITLE OF INVENTION: HCV Shuttle Replicon Vectors
; FILE REFERENCE: R0277A-PRO
; CURRENT APPLICATION NUMBER: US/60752,866
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patencin version 3.2
; SEQ ID NO 7
; LENGTH: 11509
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Nucleotide sequence of plasmid pBS-1_1a_NSSB_5'Avsi1_3'Parr11
US-60-752-866-7

Query Match      83.8%; Score 1727.8; DB 12; Length 11509;
Best Local Similarity 89.9%; Pred. No. 0;
Matches 1852; Conservative 0; Mismatches 207; Indels 0; Gaps 0;

Qy 1 ATGGCGCTATCAGGCGCTATGCTCCAGCAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60
Db 3347 ATGGCGCTATCAGGCGCTATGCTCCAGCAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3406
Qy 61 AGCTTACCGGCGGAGCAAAAACAGGTGAGAGGTGAGGTTCAATGCTGCTCAACTGCT 120
Db 3407 AGCTTACCGGCGGAGCAAAAACAGGTGAGAGGTGAGGTTCAATGCTGCTCAACTGCT 3466
Qy 121 GCCGACCTTCTTGGCAACTGTCATTTACGAGGAGTGTGTTGAGACTGTCAATGAGAGCC 180
Db 3467 ACACATCTTCTTGGCGACTGTCATTTGAGAGTGTGTTGAGACTGTCAATGAGAGTGC 3526
Qy 181 GGAAACAGAGACATGCTGCTCACTTAAGAGGTGCTGTTATCCAGATGATGATGATGATGATGATGAT 240
Db 3527 GGCTCAAGAGACCTTGGCGGCTGCTCACTTAAGAGGTGCTGTTATCCAGATGATGATGATGATGATGATGAT 3586
Qy 241 CAAGACTGATGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
Db 3587 CAAGACTGATGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3646
Qy 301 GGCTCTGAGGACCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
Db 3647 GGCTCTGAGGACCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3706
Qy 361 GGTGATGAGGAGGAGAGCTGCTTTCGCGCGGCTATCTTACTTGAAGAGCTCTCG 420

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Db 3707 GGTGATAGAGGGGATGACCTGCTTTGCCCCCGCCATTTCTATCTTGAAGGCTCTCG 3766
Qy 421 GGAGGCGCTCTGCTGTGCCCCCGAGAGCATGCGTGAAGCATATTCAGAGCCCGGTATGC 480
Db 3767 GGGGGGCTCCCTGTGTGGCCCCCGGAGACGCGGTGGGCTTATTCAGAGGCGCCGGTGTGC 3826
Qy 481 ACCCGTGAAGTGGCTAAAGCGGTGAGCTTCATCCCGTGAAGAGCTTGAAGCAACCATG 540
Db 3827 ACCCGTGAAGTGAAGCGGTGAGCTTATTCCTGTGAAGAACTTGAAGCAACCATG 3886
Qy 541 AGGTCGCCGCTGTCTCAGACAACTCTCCACAGAGAGTGCACAGAGTACCAAGT 600
Db 3887 AATATCCCGGTGTTCACGAGCAACTCTCTCCACAGAGAGTGCACAGAGTTCACAGGT 3946
Qy 601 GCCCATCTGATGCTCCACCGGAGCGGTAAAGAGCAAGAGTCCCGGCGCATACGCA 660
Db 3947 GCCCATCTGATGCTCCACCGGAGCGGTAAAGAGCAAGAGTCCCGGCTCGTACGCA 4006
Qy 661 GCTCAGGGGTACAAAGGTGTGGTGCACCCCTCGGTGTCGAACATGGGCTTTGGT 720
Db 4007 GCCCAGGGGTACAAAGGTGTGGTGCACCCCTCGGTGTCGAACGCTGGGCTTTGGT 4066
Qy 721 GCTTACATGTCGAAGGCCCATGAGGATGATCTTACATCAGAGACTGGGTGAGACAAT 780
Db 4067 GCTTACATGTCGAAGGCCCATGAGGATGATCTTACATCAGAGACTGGGTGAGACAAT 4126
Qy 781 ACTACTGAGAGCCCGATCAGATATTCACCTTACGAGAGTCTTGGCGAGCGGGTGT 840
Db 4127 ACCCATGAGAGCCCGATCAGATATTCACCTTACGAGAGTCTTGGCGAGCGGGTGT 4186
Qy 841 TCAGGGGGGTCTTATGACATATTAATTGAGAGAGTGCATCCAGAGTGCACATTC 900
Db 4187 TCAGGGGGGTCTTATGACATATTAATTGAGAGAGTGCATCCAGAGTGCACATTC 4246
Qy 901 ATCTTGGGATTTGGCACTGTCTTGAACAAGAGAGAGCGCGGGCGAGACTGTG 960
Db 4247 ATCTTGGGATTTGGCACTGTCTTGAACAAGAGAGAGCGCGGGCGAGACTGTG 4306
Qy 961 CTGCGCAGCGCTAACCCCTCGGGGCTCGTCACTGTGCCCCCATCTTAACTGAGAGTT 1020
Db 4307 CTGCGCAGCGCTAACCCCTCGGGGCTCGTCACTGTGCCCCCATCTTAACTGAGAGTT 4366
Qy 1021 GCTCTGTCACTAACCGGAGAGATCCCTTTATGGAAGGCTATCCCTTGAAGCAAT 1080
Db 4367 GCTCTGTCACTAACCGGAGAGATCCCTTTATGGAAGGCTATCCCTTGAAGGATC 4426
Qy 1081 AAGGGGGGAGACATCTCATCTTCTGCACTCAAGAAAGATGCGAGCTCGCGCA 1140
Db 4427 AAGGGGGGAGACATCTCATCTTCTGCACTCAAGAAAGATGCGAGCTCGCGCG 4486
Qy 1141 AAACGTGTGCGTGGGCGCTCAATGCGGTGCTTACTACCGGCGCTTGTATGTCTGTC 1200
Db 4487 AAGCTGTGTGCAATGGGCAATGATGCGGTGCTTACTACCGGCGCTTGTATGTCTGTC 4546
Qy 1201 ATCCGAGCAGGTGAGAGTGTGCGTGTGCGGCACTGAGCGCTTATGACCGGCTTAC 1260
Db 4547 ATCCGAGCAGGTGAGAGTGTGCGTGTGCGGCACTGAGCGCTTATGACCGGCTTAC 4606
Qy 1261 GGCGACTTGCATTCGGTGTATGACTGCAACAGTGTGTCAACCGAGACTGTCAAC 1320
Db 4607 GGCGACTTGCATTCGGTGTATGACTGCAACAGTGTGTCAACCGAGACTGTCAAC 4666
Qy 1321 CTTGACCTTACTTCACTTGAAGACATGACGCTTCCCGAGAGTGTCTTCCGCTACT 1380
Db 4667 CTTGACCTTACTTCACTTGAAGACATGACGCTTCCCGAGAGTGTCTTCCGAGACT 4726
Qy 1381 CAACGTGCGGGTGAAGCTGCGAGAGGAGCGAGGATCTTACAGATTTGTGCAACCGGG 1440
Db 4727 CAACGTGCGGGGAGAGCTGCGAGAGGAGCGAGGATCTTATGATTTGTGCAACCGGG 4786
Qy 1441 GAGCGCTTCTGAGCATGTTTGAAGTGTGCTCTGTCGAGGTATGACCGGGGTTGT 1500
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Db 4787 GAGGCGCCCTCGGATGTTCGACTGTCGCTCTCTGTGAGTGTATGACGCGGCTGT 4846
Qy 1501 GCTTGTATGAGCTTACGCCCGCGAGACCAAGTTAGGCTTACGAGCATATGAAACCC 1560
Db 4847 GCTTGTATGAGCTTACGCCCGCGAGACCTACAGTTAGGCTTACGAGCGTACATGAAACC 4906
Qy 1561 CCGGACTTCCCGTGTGCGAAGACCATTTTGAAGAGGCGCTTTTACGGGCTCT 1620
Db 4907 CCGGCGCTTCCCGTGTGCGAAGACCATTTTGAAGAGGCGCTTTTACGGGCTCT 4966
Qy 1621 ACCCATATGAGCGCCCATCTTATCCAGCAAAAGAGAGTGGGAAAACTTCTTAT 1680
Db 4967 ACTCATATATGATGCCCATTTTATCCAGCAAAAGAGAGTGGGAAAACTTCTTAT 5026
Qy 1681 CTGTGAGGTATCAAGCCACCGTGTGCGCTAGAGTCAAGCCCTCCCGGTGGAG 1740
Db 5027 CTGTGAGGTATCAAGCCACCGTGTGCGCTAGAGTCAAGCCCTCCCGGTGGAG 5086
Qy 1741 CAGATGTGGAAGTGTGATCCGTCTCAAGCCCATCTCAATGGGCAACCTCTGCTA 1800
Db 5087 CAGATGTGGAAGTGTGATCCGTCTCAAGCCCATCTCAATGGGCAACCTCTGCTA 5146
Qy 1801 TATAGACTGGCGCTGTCCAGATATGAGTCAACCTTGAAGCCAGTCAACCAATATATC 1860
Db 5147 TATAGACTGGCGCTGTCCAGATATGAGTCAACCTTGAAGCCAGTCAACCAATATATC 5206
Qy 1861 ATGACATATATGTGGCTGAGCTGAGAGTGTGCTACAGATACCTGGGTCTGTGGCGG 1920
Db 5207 ATGACATATATGTGGCTGAGAGTGTGCTACAGATACCTGGGTCTGTGGCGG 5266
Qy 1921 GTTCTGCTGCTTTGGCGCGGTATTTCTTATCCAGAGCTGCGGTATAGTATAG 1980
Db 5267 GTTCTGCTGCTTTGGCGCGGTATTTCTTATCCAGAGCTGCGGTATAGTATAG 5326
Qy 1981 ATGTCTTGTCCGGAAGCCGCAATCATATCCGACAGAGAGTCTTACCGGAGTTC 2040
Db 5327 ATGTCTTGTCCGGAAGCCGCAATCATATCCGACAGAGAGTCTTACCGGAGTTC 5386
Qy 2041 GATGAATGGAAGTGTCT 2059
Db 5387 GATGAATGGAAGTGTCT 5405

RESULT 14
US-10-559-431-1
; Sequence 1, Application US/10559431
; GENERAL INFORMATION:
; APPLICANT: BIOMERIEUX
; TITLE OF INVENTION: INSITU NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; TITLE OF INVENTION: Composition comprising the polypeptide NS3/NS4 and the polypeptide
; TITLE OF INVENTION: of HCV, expression vectors including the corresponding nucleic acid
; FILE REFERENCE: ADENOVIR
; CURRENT APPLICATION NUMBER: US/10/559,431
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent version 3.1
; SEQ ID NO 1
; LENGTH: 2844
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence coding for NS3NS4
; NAME/KEY: CDS
; LOCATION: (1) .. (2844)
; OTHER INFORMATION:
US-10-559-431-1

Query Match 67.2%; Score 1384.4; DB 6; Length 2844;
Best Local Similarity 79.5%; Pred. No. 0;
Matches 1637; Conservative 0; Mismatches 421; Indels 0; Gaps 0;
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QY 1 ATGGGCGCTATACGAGCGCTTATGCCAGACAGACAGAGGCGCTTTTGGGATGATATACACC 60
 Db 1 ATGGGCGCTATACGAGCGCTTATGCCAGACAGACAGAGGCGCTTTTGGGATGATATACACT 60
 QY 61 AGCTTGAACCGGCGGAGACAAAAACGAGGTGAGGGTTCAGATCGTGTCAACTGCT 120
 Db 61 AGCTTGAACCGGCGGAGACAAAAACGAGGTGAGGGTTCAGATCGTGTCCACCGCA 120
 QY 121 GCCGACCTTTTCTTGGCAACCTGCAATTAACGGGGTGTGTGGACGTGTCAATGAGACC 180
 Db 121 AGCGAATCTTCTCTGGCGACCTGCGTCAATGGCGTGTGTGGACCGTGTCAATGAGTGC 180
 QY 181 GGAACAGGACCATTTGCGCTACCTAAGGCTCCTTTATCCAGATGATACCAATGAGAC 240
 Db 181 GCGTGAAGACCTTGGCGCGGCGGAGGCTCAATACCAATGATACCAATGATAGAC 240
 QY 241 CAAAGACTTGTAGGCTGGCGCGCTCCCAAGGTGCGCGCTCATTAACCAATGACACTTGC 300
 Db 241 CAGGACCTGTGGCTGGCGCGCGCGCGCGCGCGCTCATGACACCGTGCACCTGC 300
 QY 301 GCGTCTCGGACCTTTAATCTGTGTCAAGAGGACCGCGATGTATTCCTGTGCGGACGG 360
 Db 301 GCGACCTCGGACCTTTAATCTGTGTGTCAAGAGGACCGCGATGTATTCCTGTGCGGACGG 360
 QY 361 GGTGATGGAGGGGAGCGCTTGTGCGCGCGCGCTATCTTATCTTGAAGGCTCTCG 420
 Db 361 GCGGACAGAGGGGAGGCTTACTCTCTCTAGGCGCGCTCTTACCTGAAGGCTCTCTCG 420
 QY 421 GGAGGCGCTTGTGTGCGCGCGAGACATGCGGTATGAGCATTTGAGACCGCGGTATGC 480
 Db 421 GGTGACACACTGTCTTGGCGCTTGGGGGACGTTGTAAGGATCTTCCGGCTGTGTGTGC 480
 QY 481 ACCCGTGAAGTGGCTTAAGGCGGTGACCTTCAATCCCGGTAGAGAGCTTGAAGACCAATG 540
 Db 481 ACCCGGGGGGTTCAGAAAGCGGTGACCTTCAATCCCGGTAGAGAGCTTGAAGACCAATG 540
 QY 541 AGGTCCCGGCTGTTCAGACAACTCTCCGACAGAGTGGCGGAGTACCAAGTGC 600
 Db 541 CGGTCTCGGCTTTCAGACAACTCTCTCCGCGCGGTACCGGACATTCGCAAGTGC 600
 QY 601 GCCCACTGATGCTCCCAACCGGAGCGGTAAAGAGACCAAGTTCGCGCGCATATACGA 660
 Db 601 GCAATTTTACAGCGCTCCCACTGGAGCGGCAAGAGACCAAGTGCCTGCATATGGA 660
 QY 661 GCTCAGGGCTAACAGGTGTGTGCTCAACCCCTCGTGTCTGCAACAATGAGCTTTGCT 720
 Db 661 GCCCAAGGGTAAAGAGTGTGTGCTCAACCCCTCGTGTCTGCAACAATGAGCTTTGGA 720
 QY 721 GCTTACATGTCCAAAGGCCATGGAATTGATCTCTTAATGAGAGCTGGGTGAGACAT 780
 Db 721 GGTATATGTCCAAAGGCATGAGCATGAGCTTAACATGAAGTGGGTGAGACAT 780
 QY 781 ACTTATGAGGAGCGGATCACTGATTCACCTACGGAAGTTCCTTGGCGAGCGGGTGT 840
 Db 781 ACCAGGGGGGCGGCGCATCACTGATTCACCTATGGAAGTTCCTTGGCGAGCGGTGTGATGC 840
 QY 841 TCAGAGGGGTGTTATGACATTAATATTGTGACGAGTGCACCTGAGTCAACGATCC 900
 Db 841 TCCGGGGGGGCGCTTATGACATTAATATTGTGACGAAATGCGCACTCAACTGAGCAACC 900
 QY 901 ATCTTGGGATGGACATGTCTTGAACGAAGAGACCGCGGGGGCGAGATGACTGTG 960
 Db 901 ATCTTGGGATGGACATGTCTTGAATCAGGAGAGACCGGTGAGCGGGGTCTGTCTG 960
 QY 961 CTGCGCACCGCTACCCCTCGGGCTCCGTCATGTCGCTGCTTCACTTACATCGAGAGGTT 1020
 Db 961 CTGCGCACCGCTACCGCTCCGGGATGATCACTGTCGCAACCCCACTTCAAGAGAGTG 1020
 QY 1021 GCTGTGTCCACTTACCGGAGAGATCCCTTTTATAGGAGGCTTATTCCTTGAAGCAAT 1080
 Db 1021 GCGCTGTCCAAACTGGGAGAGATTCCTTCTTATGGAAAGCATCCCACTTGAAGGCAATC 1080
 QY 1081 AAGGGGGGAGACATCTCATCTTGTGCCACTGAAAGAAAGTGGAGCAGAGCTCGCGCA 1140

Db 1081 AAGGGGGGAGACATCTATCTTGTGCCATTCGAAAGAAAGATGAGAGCTCGCGCA 1140
 QY 1141 AAACGTGTGCGGTTGGGCGTCAATCCGCTTACTTCAACCGCGCTTGTATGTCCGTC 1200
 Db 1141 AAGCTGAAGGCGCTCGACTCAATGCTGTAGGTATTCACGGGGGTCTCATGTGTCCGTC 1200
 QY 1201 ATCCGACCAAGTGAAGTGTGTGTGCGTGAATGACGCGCTCATGACCGGCTTTTACC 1260
 Db 1201 ATACGACCTAGGAGAGAGTGTGTGTGTGCGTGAAGAGAGCTTATGACGGGCTTTTACC 1260
 QY 1261 GCGCACTTGCATTCGAGTATGACTGCAACAGTGTGTACCCAGACAGTGCATTCAGC 1320
 Db 1261 GCGCACTTGCATGATGATGACAGCAACATGTGTACCCAGACAGTGTGTTCAGC 1320
 QY 1321 CTGACCTTACCTTCAACATTAAGCAATCAACGCTTCCCAAGATGTGTCTCCGTAAT 1380
 Db 1321 TTGATTCACCACTTCAACATTAAGCAACACCGTCCCAAGACCGGCTGTGCGCTGC 1380
 QY 1381 CAACGTGGGGGTAGGACCTGGAGAGGAGGACGAGGATCTACAGATTGTGSCACCGGG 1440
 Db 1381 CAGCGGAGAGGTAGGACCTGGAGAGGAGGAGTGCATCTACAGATTGTGCTTCAAGGA 1440
 QY 1441 GAGCGTCTTGTGAGTGTGATCTGTGTGTCTGTGAGTGTATGACGCGGATGT 1500
 Db 1441 GACGCGCTTCAAGGATGTGATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1500
 QY 1501 GCTTGTATGAGCTTACGCGCGCGAGACCAAGTTAGGCTTACGAGCATATGAAACACC 1560
 Db 1501 GCTTGTATGAGCTTACGCGCGCGAGACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1560
 QY 1561 CCGGACCTTCCGTTGTGCAAGACCACTTGAATTTTGGAGGGGCTTTTACGGGTCTC 1620
 Db 1561 CCGGAGTGTGCGTGTGCAAGACCACTTGAAGTTTGGAGGGGCTTTTACGGGTCTC 1620
 QY 1621 ACCCATATGAGCGCGCACTTCTATCCAGACCAAGAGAGTGGGAAAACTTCCCTAT 1680
 Db 1621 ACCCATATGATGATGCCCATCTTCTGTCTCCAAACAGAGAGAGAGCACTTCCCTATC 1680
 QY 1681 CTGTAGCGGTACCAAGCCACGCTGTGCGTGAAGCTCAAGCCCTTCCCGTGTGGAC 1740
 Db 1681 CTGTGTGATACCAAGCCACGCTGTGCGCTGAGGCTCAAGGCTCTCATCTGTGTGGAT 1740
 QY 1741 CAGATGTGAAGTGTGTATCCGTCTCAAGCCACCTTCCATGAGGCGCAACCTCTGCTA 1800
 Db 1741 CAATGTGAAGTGTCTATAGGCTTAACTTACGTGACAGGCGCAACCTCTGCTG 1800
 QY 1801 TATGACCTGGGCGCTGTCCAGATGAAGTCAACCTGACGACCCAGTCCAAAGTATATC 1860
 Db 1801 TATAGGCTAGAGGCCGTTTCAAAATGATACCTTCAACATCCATCAACAAATTCGTC 1860
 QY 1861 ATGACATATGTTCGCTGACCTGAGAGTCTGACAGATCTGTGGGTCTGTGGCGGC 1920
 Db 1861 ATGGCATGATGTTCGCGCGAGCTGAGAGGTGTGCTATGACACTGTGGGTGTGTAAGCGGA 1920
 QY 1921 GTTCTGCGCTTGTGGCGCGGATGCTTATCAAGGCTGTGTGTCTATATGATGATG 1980
 Db 1921 GTCTTGTGACGCTGTGGCGGATATGCTTGAACACCGGTAGGTGTCTATGATGATG 1980
 QY 1981 ATGTCTTGTCCGGAAGCGGCAATCAATCCGACAGGAGAGTCTCTTACCGGAGTTC 2040
 Db 1981 ATCATTTGTTCGAGAGGCGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2040
 QY 2041 GATGAATGAAAGAGTGC 2058
 Db 2041 GATGAATGAAAGAGTGC 2058

RESULT 15
 US-10-559-431-1
 ; Sequence 1, Application us/10559431
 ; GENERAL INFORMATION:
 ; APPLICANT: BIOMERIEUX

APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
TITLE OF INVENTION: Composition comprising the polypeptide NS3/NS4 and the polypeptide of HCV, expression expression vectors including the corresponding nucleic acid
TITLE OF INVENTION: their therapeutic use
FILE REFERENCE: ADEMOVIR
CURRENT APPLICATION NUMBER: US/10/559,431
CURRENT FILING DATE: 2005-12-05
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 2844
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: sequence coding for NS3NS4
NAME/KEY: CDS
LOCATION: (1)..(2844)
OTHER INFORMATION:
US-10-559-431-1

Query Match 67.2%; Score 1384.4; DB 7; Length 2844;
Best Local Similarity 79.5%; Pred. No. 0;
Matches 1637; Conservative 0; Mismatches 421; Indels 0; Gaps 0;

QY 1 ATGGGCGCTATACGCGCTATGCGCCGAGAGCAAGGCGCTTTGGGATGATTAATCAAC 60
DB 1 ATGGGCGCTATACGCGCTATGCGCCGAGAGCAAGGCGCTTTGGGATGATTAATCAAC 60
QY 61 AGCTTGACCGCGCGGAGCAAAAACAGTGAGGAGTGAGGTTCAATCTGTCAACTGCT 120
DB 61 AGCTTGACCGCGCGGAGCAAAAACAGTGAGGAGTGAGGTTCAATCTGTCAACTGCT 120
QY 121 GCGGACACTTTCTTGGCAACCTGATTAACGGGGTGTGTGAGACTGTCTACCATGAGGC 180
DB 121 GCGGACACTTTCTTGGCAACCTGATTAACGGGGTGTGTGAGACTGTCTACCATGAGGC 180
QY 121 AGCGAATCTTCTTGGCAACCTGATTAACGGGGTGTGTGAGACTGTCTACCATGAGGC 180
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QY 181 GGAAAGAGGACATTCGTCACCTTAAGGTCCTGTTATCCAGATGATGACCAATGAGAC 240
DB 181 GGAAAGAGGACATTCGTCACCTTAAGGTCCTGTTATCCAGATGATGACCAATGAGAC 240
QY 181 GCGTGAGAGACCTTGCG 240
DB 181 GCGTGAGAGACCTTGCG 240
QY 241 CAAGACCTGTGAGCTGAGCGCGCTCCCAAGGTGCCGCTCAATTAACCATGACCTTGC 300
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QY 301 GCGTCTCGGACCTTTAATCTGTGATGAGAGGCAAGCGGATGATCTTCTGTGGCGGAG 360
DB 301 GCGTCTCGGACCTTTAATCTGTGATGAGAGGCAAGCGGATGATCTTCTGTGGCGGAG 360
QY 361 GGTGATGAGGAGGAGGAGCTGCTGCTTGGCGCGCGCTATCTTAACTTGAAGGCTCTGC 420
DB 361 GGTGATGAGGAGGAGGAGCTGCTGCTTGGCGCGCGCTATCTTAACTTGAAGGCTCTGC 420
QY 361 GGTGATGAGGAGGAGGAGCTGCTGCTTGGCGCGCGCTATCTTAACTTGAAGGCTCTGC 420
DB 361 GGTGATGAGGAGGAGGAGCTGCTGCTTGGCGCGCGCTATCTTAACTTGAAGGCTCTGC 420
QY 421 GAGAGCGCTCTGCTGTGCGCGGAGGACATGCGGATGAGGATTAATGAGCGCGGATGAG 480
DB 421 GAGAGCGCTCTGCTGTGCGCGGAGGACATGCGGATGAGGATTAATGAGCGCGGATGAG 480
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DB 421 GGTGAGGACATGCTTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480
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DB 541 CCGTCTCGGATGTTTCAAGACATCTGCGGACGAGAGTGGCGCGGAGCTACCAAGTG 600
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DB 601 GCGGACCTGATGCTTCCCAAGCGGAGGATGAGAGCAAGGATGAGGATGAGGATGAGG 660
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DB 601 GCGGACCTGATGCTTCCCAAGCGGAGGATGAGAGCAAGGATGAGGATGAGGATGAGG 660
QY 661 GCTCAAGGCTCAAGGATGCTGCTGCTCAACCCCTCGCTTGTGCAATGAGGCTTTGGT 720
DB 661 GCTCAAGGCTCAAGGATGCTGCTGCTCAACCCCTCGCTTGTGCAATGAGGCTTTGGT 720
QY 661 GCGGACCTGATGCTTCCCAAGCGGAGGATGAGAGCAAGGATGAGGATGAGGATGAGG 720
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QY 721 GCTTACATGCTCCAGGCGCCATGAGATGATGATCTTAACATGAGGATGAGGATGAGCAATT 780
DB 721 GCTTACATGCTCCAGGCGCCATGAGATGATGATGATCTTAACATGAGGATGAGGATGAGCAATT 780
QY 781 ACTATGCGAGCGCGGATGAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
DB 781 ACTATGCGAGCGCGGATGAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
QY 781 ACCAGGCGCGCGCGGATGAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
DB 781 ACCAGGCGCGCGCGGATGAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
QY 841 TCAGGCGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
DB 841 TCAGGCGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
QY 901 ATCTTGGGACATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
DB 901 ATCTTGGGACATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
QY 901 ATCTTGGGACATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
DB 901 ATCTTGGGACATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
QY 961 CTGCGCACCGGACCGCTCGGCGGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
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QY 1021 GCTGCTGACATGAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
DB 1021 GCTGCTGACATGAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
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QY 1081 AAGGCGGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140
DB 1081 AAGGCGGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140
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DB 1141 AAGGCGGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140
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QY 1201 ATCCGACGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260
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QY 1261 GCGGACCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320
DB 1261 GCGGACCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320
QY 1321 TTGATGACGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380
DB 1321 TTGATGACGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380
QY 1381 CAAGCTGCGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
DB 1381 CAAGCTGCGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
QY 1441 GAGGCTGCTTGTGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1500
DB 1441 GAGGCTGCTTGTGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1500
QY 1501 GCTTGTGATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
DB 1501 GCTTGTGATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
QY 1561 CCGGACCTTGTGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
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DB 1621 ACCGACATGAGCGGACCTTGTGAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
QY 1681 CTGAGGATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740
DB 1681 CTGAGGATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740
QY 1741 CAGATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1800
DB 1741 CAGATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1800
QY 1801 TATAGAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1860
DB 1801 TATAGAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1860

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Db 1801 TATAGCTAGAGAGCGGTTCAAAATGAGANTCAACCTCAGACATCCCATACCAATTCGTC 1860
Qy 1861 ATGACATGTAATGTCGGCTGACCTGGAGAGTCGTACAGAGTAACCTGGGTGCTCGTTGGCGGC 1920
Db 1861 ATGCAATGATGTCGGCGCCGACCTGGAGAGTCGTCACTAGCACCTGGGTGCTGGTAGGCGGA 1920
Qy 1921 GTTCTGGCTGCTTTGGCGCGGATATGGCTATCCACAGGCTGGGTGTCATAGTAGTAGG 1980
Db 1921 GTCTTGACGCTCTGGCGCATATTGCTGACACCGGTAGTGTGTCATTGTGGGTAGG 1980
Qy 1981 ATTGCTTGTCCGAAAGCCGCAATCATACCCGACAGGGAAGTCTCTACCGGAGTTTC 2040
Db 1981 ATCATTTTGTCCGGAGAGCCGCTGTGTTCCCGACAGGGAAGTCTCTACCGGAGTTTC 2040
Qy 2041 GATGAATGGAAGAGTGC 2058
Db 2041 GATGAATGGAAGAGTGC 2058
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Search completed: February 7, 2006, 20:35:36
Job time : 441 secs

Bank (12/1)